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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Gapop 10.0 , Gapext 1.
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

#### Result O O O 000 358.8 358.8 358.8 358.1 130 127.2 126.8 117.4 116.4 11 53.4 52.2 51.8 51.8 50.4 50.2 49.2 48.8 56 67 Query Match $\begin{array}{c} 667 \\ 644.3 \\ 88888999990.0.1 \\ 1.01 \\ 1.02 \\ 1.03$ . 9 3 198728 3 198728 0 10592 0 181581 0 181581 8 10428 8 12059 2220 2313 100906 1250 3082 16812 10000 15247 12141 7 12141 7 12141 347550 2225 38571 1785 81624 109741 37093 1971 2187 2187 Length 2037 1810 1994 2002 ВB 6688312 **w & & & & & & & & & &** 10 10 AX356174 AA7326 AR097968 AR097968 AR145810 AX356172 HSA237672 HSA2 AF181967 AY050434 AF370515 AF441241 AC099763 AC004005 SPAC56F8 AX069359 AR144956 HSU09806 A47328 AY070034 AF174486 ATH245414 AY122922 MMMTHFR06 AL606929 AE006058 AC113917 AE006357 AR097969 AR145811 AX050441 AF181966 \_02 ujj849 Caenorhabdi AF441241 Synthetic AC099763 Caenorhab AC004005 Arabidops Z69728 S.pombe chr AX069359 Sequence AR144956 Sequence AR144956 Sequence AR144956 Sequence AR144956 Sequence AR147328 Sequence AR145811 Sequence AR145811 Sequence AR145815 Sequence AR145810 Sequence AR160767 Rattus norv Z72647 S.cerevisia Continuation (3 of AE001408 Suchera AR1646057 Ralstonia AR105939 Musmuscu AL606929 Mouse DNA AE006058 Pasteurel AC113917 Rattus no AE006357 Lactococc AE005886 Caulobact AF181967 Arabidops AY050434 Arabidops AF370515 Arabidops AJ245414 Arabidops AY122922 Arabidops Description AF174486 Zea mays AX452358 Arabidops Arabidops Sequence

## ALIGNMENTS

REFERENCE	SOURCE	ACCESSION	RESULT 1 AF181967 LOCUS DEFINITION
AUTHORS	ORGANISM	VERSION	
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  1 (bases 1 to 1897) Roje,S., Wang,H., McNeil,S.D., Raymond,R.K., Appling,D.R.,	Arabidopsis thaliana. Arabidopsis thaliana Arabidopsis thaliana: Streptophyta: Embryophyta; Tracheophyta;	MKNA, COMPLETE COS. AF181967 AF181967.1 GI:5911426	AF181967 1897 bp mRNA linear PLN 13-DEC-1999 Arabidopsis thaliana methylenetetrahydrofolate reductase MTHFR2

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                                       CTCGTTCTTTACCCTGGAGACGCCCTGCAAATGTTTTCCGTACTAAGGAAGATGTGCGCC
                                                           CTAGGTCCTTACCTTGGAGACGCCCTGCAAATGTTTTCCGGTGTTAAAGAAGATGTCCCGTC
                                                                                                                          TGGAGAAATCTGCATTGGCAATACTAATGAACCTTGGCCTAATTGAAGAGTCCAAAGTTT
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Submitted (31-AUG-1999) Horticultural Sciences,
Submitted unil Road, Gainesville, FL 32611-0690,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shachar-Hill,Y., Bohnert,H.J. and Hanson,A.D. Isolation, characterization, and functional expression of cDNAs
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G1QNVLALRGDEPHGODKFVOVEGGFDCALDLVNHTRSKYGDYEGITVAGYEBAHPDV
IGENGLASNAVGSDLEYLKKKIDAGADLIVPLHTRDIFLKFVNDCRGISISCHP
PG1MPINNYRGEAVQSDLEYCKKIPVEVMAALETPLFVDUREAVRAYGIHLGTGISCPIV
PG1MPINNYRGEAVGSTALLWILLDHALETPLFVDUREAVRAYGIHLGTREMCKKMLA
HGVKSLHLYTLMMEKSALAILMNLGMIDESKISFLPWRRPANVERTREDVRFPIFMAN
RPKSYISRTKGMEDFPQGRWGDSRSASYGALSDHQFSRPARDKKLQQEMVVPLKSVE
DIQEKFRELCLGNLKSSEWSELDGLQPETRIINEQLIKVNSKGFLTINSQPSVNAERS
DSPTVGWGGPYGYVYQKAYLEFFCSKEKLDAVVEKCKALPSITYMAVNKGEQWYSNTA
QADVNAVTWGVFPAKEIIQPTIVDPASFNVWKDEAFETWSRSMANLYPEADPSRNLLE
EVKNSYYLVSLIVENDYINGDIFAVFADL*

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Location/Qualifiers
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/protein_id="AAD55788.1"
/db_xref="GI:5911427"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /function="catalyzes the reduction of 5,10-methylenetetrahydrofolate (CH2-THF) 5-methyltetrahydrofolate (CH3-THF)"
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/codon_start=1
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/db_xref="taxon:3702"
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                                                                                                                                                                                                                                                                                             The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFI CDNAs: Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Koesema, E., Meyers, M.C., Banh, J. Bowser, L., Dale, J.M., Goldsmith, A.D., Jiang, P.X., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Mguyen, M., Onodera, C.S., Palm, C.J., Pham, P.K., Quach, H.L., Southwick, A., Tang, C.C., Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Davis, R.W., Theologis, A., and Ecker, J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 1917)
Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Koesema, E., Meyers, M.C.,
Banh, J., Bowser, L., Carninci, P., Dale, J.M., Goldsmith, A.D.,
Banh, J., Bowser, L., Carninci, P., Dale, J.M., Goldsmith, A.D.,
Hayashizaki, Y., Ishida, J., Jiang, P.X., Jones, T., Kamiya, A.,
Kariln-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lih, J., Liu, S.X.,
Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J.,
Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J.,
Pham, P.K., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A.,
Tang, C.C., Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S.,
Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.
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Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Koesema, E., Meyers, M.C., Bahh, J., Bowser, L., Carninci, P., Dale, J.M., Goldsmith, A.D., Hayashizakl, Y., Ishida, J., Jiang, P.X., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Pham, P.K., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; are endicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL CDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida, Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (02-AUG-2001) Salk Institute Genomic Analysis Laboratory (SIGnAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037
                                                                                                                                                                       this work. Shinozaki, K. (RIKEN contributed equally to this work
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis cDNA clones Unpublished
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                                                                                                                                                                                                                                         (SSP/Salk) and Seki,M.
/organism="Arabidopsis
/db_xref="taxon:3702"
/chromosome="2"
                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                       (RIKEN GSC) contributed equally GSC) and Ecker, J.R. (SSP/Salk) k as PIs.
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                                                                                                                                                                            AGTTCATGCGGCCACGTG
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AF370515
Arabidopsis thaliana putative methylenetetrahydrofolate reductase (At2g44160; F6E13.29) mRNA, complete cds.
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GIQNVLALRGDPPHGQDKFVQVEGGFDCALDLVNHIRSKYGDYFGITVAGYPEAHPDV
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/protein_id="AAK91450.1"
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/translation="MKVIDKIQSLADEGKTAFSFEFFPPKTEDGVDNLFERMDRMVAY
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Pred. No.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Southwick, A. (SSP/Stanford) and Seki, M. (RTKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Davis, R.W. (SSP/Stanford) contributed equally to this work as PIs. Location/Qualifiers
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Submitted (17-APR-2001) DNA Sequencing and Technology Center,
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DIQEKFKELCLGNLKSSPWSELDGLQPETRIINEQLIKVNSKGFLTINSQPSVNAERS
DSPTVGWGGPVGYVYQKAYLEFFCSKEKLDAVVEKCKALPSITYMAVNKGEQWVSNTA
                                                                                                                                                                                                                                                                                                                                                                                                /product="putative methylenetetrahydrofolate reductase" /protein_id="AAK43892.1" /db_xref="GI:13877629" /db_xref="GI:13877629" /translation="MKUDKIOSLADEGKTAFSFEFFPPKTEDGVDNLFERMDRMVAY GPTFCDITWGAGGSTADLTLDIASRMQNVVCVESMMHLTCTNMPVEKIDHALETIRSN GIQNVLALRGDPHHGQDKFYQVEGGFDCALDLVNHIRSKYGDYFGITVAGYPEAHPDV
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PGIMPINNYRGFLRWTGFCKTKIPVEVMAALEPIKDNEEAVKAYGIHLGTEMCKKMLA
HGVKSLHLYTLNMEKSALAILMNLGMIDESKISRSLFWRRPANVFRTKEDVRPIFWAN
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91. .1875
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/note="This clone is i
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/db_xref="taxon:3702"
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                                                                                                                                   Direct Submission
Submitted (27-JUL-1999) Ravanel S., DBMS
CEA-Grenoble, 17, rue des Martyrs, 38054
Location/Qualifiers
                                                                                                                                                                                                                            Ravanel,S., Rebeille,F. and Douce,R. Folate metabolism in higher plants: cloning of a cDNA for 5,10-methylenetetrahydrofolate reductase in Arabidopsis thaliana
                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II, Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 2037)
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Arabidopsis thaliana
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                                                                                 /organism="Arabidopsis
/db_xref="taxon:3702"
68. .1852
/gene-"MTHFR1"
/EC_number-"1.5.1.20"
/function="reduction of methylenetetrahydrofolate to methyltetrahydrofolate"
                                                                  /gene-"MTHFR1"
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GPTFCDITWGAGGSTADLTLDIASRMGSVVCVESMMHLTGTINKPUEKIDHALETIRSN
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IGENGLASNEAYOSDLEYLKKIDAGADLIVTQLFYDTDIFLKFVNDCRQIGISCPIV
GGENGLASNEAYOSDLEYLKKIDAGADLIVTQLFYDTDIFLKFVNDCRQIGISCPIV
FGIMPINNYRGFLRMTGFCKTKIPVEVMAALEFIKDNEEAVAKGIHLGTEMCKKMLA
HGVKSLHYTLNMEKSALAILMNLGALDESKISRSLFWFRANVFFTYEBDVRDTFMAAL
HGVKSLHYTLNMEKSALAILMNLGALDESKISRSLFWFANVFRYKENAL
HGVKSLHYTLNMEKSALAILMNLGALDESKISRSLFWFANVFRYKENAL
HGVKSLHYTLNMEKSALAILMNLGALDESKISRSLFWFANVFRYKENAL
HGVKSLHYTLNMEKSALAILMNLGALDESKISRSLFWFANVKKLQQEMVVPLKSVE
RPKSYISRTKGWEDFFQGRWGDSRSASYGALSDHQFSRPRARDKKLQQEMVVPLKSVE
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DSPTVGWGGPVGYVYQKAYLEFFCSKEKLDAVVEKCKALPSITYMAVNKGEQWVSNTV
QADVNAVTWGVFPAKEIIQPTIVDPASFNVWKDEAFETWSRSWANLYPEADPSRNLLE
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/product="methylenetetrahydrofolate
/protein_id="cAB53783.1"
/db_xref="GI:5823583"
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Lee, J. M., Deng, J.M., Hsuan, V.W.

Lee, J. M., Quach, H.L., Tang, C.C., Toriumi, M., Wu, H.C., Yu, G.,

Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y.,

Lishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J.,

Kim, C., Lam, B., Lin, J., Miranda, M., Narusaka, M., Nguyen, M.,

Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A.,

Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFL cDNAs: Yamada,K., Chan,M.M., Chang,C.H., Dale,J.M., Deng,J.M., Hsuan,V.W., Lee,J.M., Quach,H.L., Tang,C.C., Toriumi,M., Wu,H.C., Yu,G., Bowser,L., Chen,H., Cheuk,R., Jones,T., Karlin-Neumann,G., Kim,C., Lam,B., Lin,J., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R. and Theologis,A.
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The RIKEN Genomic Sciences Center (GSC) members carried out collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki, M., Narusaka, M., isi Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yamada,K., Chan,M.M., Chang,C.H., Dale,J.M., Deng,J.M., Hs
Lee,J.M., Quach,H.L., Tang,C., Toriumi,M., Wu,H.C., Yu,G.,
Bowser,L., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y.,
ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J
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/db_xref="G1:2169667"
/tdb_xref="G1:2169667"
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HGITISLHLYTLNDKSAJIGILKNIGLIDESKISSLDWRFPAKNYFRTKEDVRPITWAN
RPKSYISRTKGWNDFPHGRWGDSHSAAYSTLSDYQFARPKGRDKKLQQEWVPIKSIE
DVQEKFKELCIGNIKSSPWSELDGLQPETKIINEQLGKINSNGFLTIINSQPSVNAAKS
DSPAIGWGGPGGYVYQKAYLEFFCSKDKLDTLVEKSKAFPSITYMAVNKSENWVSNTG
       /gene="At3g59970"
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                                                                                                                                             ESDVNAVTWGVFPAKEVIQPTIVDPASFKVWKDEAFEIWSRSWANLYPEDDPSRKLLE
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Roje, S. and Hanson, A.D.
Direct Submission
                                                                                                                                Roje,S., Wang,H., McNeil,S.D., Raymond,R.K., Appling,D.R., Shachar-Hill,Y., Bohnert,H.J. and Hanson,A.D. Shachar-Hill,Y. Bohnert,H.J. and Hanson,A.D. Shachar-Hill,Y. Bohnert,H.J. and Hanson,A.D. expression of cDNAs Isolation, characterization, and functional expression of cDNAs encoding NADH-dependent methylenetetrahydrofolate reductase from
                                                                                                                                                                                                Arabidopsis thaliana.
Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                       ACCCACATGGGCGTTGGGGTGATTCCTGTAATCCATCATATGGTGCATTATCTGATTATCT
                                                                                                                                                                                                                                                                                                       CAATCTTTTGGGCAAATCGACCAAAAAGCTACATATCAAGGACCATAGGATGGGATCAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                   CTAGGTCCTTACCTTGGAGACGCCCTGCAAATGTTTTCCGTGTTAAAGAAGATGTCCCGTC
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          AGTTTGCGCGCCCA 1181
                                                                         AGTTCATGCGGCCA 554
                                                                                                                                  TCCCACATGGACGTTGGGGTGATTCACACAGTGCAGCATACAGTACACTTTCGGATTATC
                                                                                                                                                                                                                                                                  CAATTTTCTGGGCAAACCGTCCAAAGAGCTACATATCTAGAACAAAGGGCTGGAATGACT
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GIQNVLALRGDPPHGODKFVQVEGGPAQALDLVNHIRSKYGDYEGITVAGYPERAHPDV
IEADGLATPESYQSDLAYLKKKVDAGADLIVTQLFYDTDIFLKFVNDCRQIGINCPIV
PGIMPISNYKGFLRMAGFCKTKIPAELTAALEPIKDNUBAVKAYGHHFATEMCKKILA
HGITSLHLYTLNVDKSAIGILMNLGLIDESKISRSLPWRRPANVFRIKEDVRPIFWAN
RPKSYISRTKGNNDFPHGRWGOSHSAAYSTLSDYQFARPKGRDKLQQEWVPLKSIE
DVQEKFKELCIGNLKSSPWSELDGLQPETKIINEQLGKINSNGFLTINSQPSVNAAKS
DSPAIGWGGPGGYYYQKAYLEFFCSKDKLDTLVEKSKAFPSITYMAYNKSEMWYSNTG
ESDVNAVTWGYFPAKEVIQPTIVDPASFKVWKDEAFEIWSRSWANLYPEDDPSRKLLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hull Road, Gainesville, FL Location/Qualifiers
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/translation="MKVVDKIKSVTEQGQTAFSFEFFPPKTEDGVENLFERMDRLVSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="methylenetetrahydrofolate reductase MTHFR1"
/protein_id="AAD55787.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Arabidopsis thaliana"
/db_xref="dbEST:W43486"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="NADH-dependent"
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78.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 358.8; | Pred. No. 1.5e | O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.5e-80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32611-0690, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yamada,K. (SSP/PGEC) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGEC) contributed equally to this work as PIs. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL CDMs: Yamada,K., Banh,J., Chang,C.H., Chang,E. Dale,J.M., Goldsmith,A.D., Lee,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Yu,S., Bowser,L., Chen,H., Cheuk,R., Jones,T., Yamamura,Y., Xu,G., Yu,S., Bowser,L., Chen,H., Cheuk,R., Jones,T., Karlin-Neumann,G., Kim,C., Lam,B., Lin,J., Meyers,M.C., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Davis,R.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (12-DEC-2001) Plant Gene Expression Center, 800 Bu
Street, Albany, CA 94710, USA
RIKEN Genomic Sciences Center (GSC) members carried out the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Satou,M., Seki,M., Shinn,P., Southwick,A., Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Goldsmith,A.D., Lee,J.M., Quach,H.L., Toriumi,M., Yu,G., Bowser,L. Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B., Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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Yamada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Chung, M.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ecker, J.R. and Theologis, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hayashizaki,Y. and Shinozaki,K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
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                                                                                                                               /gene="At3g59970"
83. .1861
                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/chromosome="3"
                                                                                                                                                                                                                                                                                                ecotype:
/evidence=experimental
/product="putative met
                                                                                                                                                                                                                                                                                             (FLC-1) as a BamHI/XhoI insert.
ecotype: Columbia"
                                                                                                                                                                                                                                                                                                                                                         /clone="RAFL09-25-L11 (R18407)"
/note="This clone is in a modified pBluescript vector
                                                               /codon_start=1
                                                                                                    /gene="At3g59970"
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800 Buchanan

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RESULT 8
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Matches 432;
    ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                             CAATTTTCTGGGCAAACCGTCCAAAGAGCTACATATCTAGAACAAAGGGCTGGAATGACT
                                                                                                                                                                                                                                                                                                                                                                                                     CAATCTTTTGGGCAAATCGACCAAAAAGCTACATATCAAGGACCATAGGATGGGATCAAT 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTAGGTCCTTACCTTGGAGACGCCCTGCAAATGTTTTCCGTGTTAAAGAAGATGTCCGTC
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Zea
Zea
                                                         AF174486 2225 bp mRNA linear
Zea mays methylenetetrahydrofolate reductase mRNA,
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AF174486.1 GI:5802605
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//db_xref="GI:17979047"
//db_xref="GI:17979047"
//db_xref="GI:17979047"
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/Franslation="MKVUDKIKSVTEQGQTAFSFEFFPPKTEDGVENLFERNDRLYSY
GPTFCDITWGAGGSTADLTLEIASRMQNVICVETMMHLTCTNNPIEKIDHALETIRSN
GIQNVLALKGDPPHGQDKFVQVEGGFACALDLVNHIRSKYGDYFGITVAGYPEAHPDV
IEAHGLAFDESYQSDLAYLKKYUDAGADLIVTQLFFUDDIFLKFVNDCRQIGINCPIV
PGIMPISNYKGFLRMAGFCKTKIPAELTAALEPIKDNDEAVKAYGIHFATEMCKKILA
HGITSLHLYTLNVDKSAIGILMNLGLIDESKISRSLPMRPAAVFRTKEDVRPIFWAN
RFKSYISRFRGWANDFPHGRWGDSHSAAYSTLSDYQFARAFKGRKKLQOGWVPLKSIE
DVQEKFKELCIGHLKSSPWSELDGLQPETKIINEQLGKINSNGFLTINSQPSVNAAKS
DSPALGWGGGGYVYQKAYLIEFFCSKDKLDTLYEKSKAFPSIITYMAYNKSENWYSNTG
ESDVNAVTWGQVFPAKEVLQDTUTQPASFKVWKDEAFEIWSRSWANLYPEDDPSRKLLE
ECSDVNAVTWGVFPAKEVLQDTUTQPASFKVWKDEAFEIWSRSWANLYPEDDPSRKLLE
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/gene="At3g59970"
/dene= 450 d
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D; Mismatches 122;
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301 882 241 822 181 762

TGGAGAAATCTGCATTGGCAATACTAATGAACCTTGGCCTAATTGAAGAGTCCAAAGTTT

360 941 881 240 821

AAATGTGCAAAAAGATTTTAGCTCATGGAATTAAGACATTGCATCTTTATACACTAAATA TAGATCCTATCAAAGACAATGAGGAGGCTGTTAGACAATATGGAATCCACCTTGGAACTG TAGAGCCTATCAAGGACAATGAAGAAGCTGTCAAGGCTTATGGAATTCACCTGGGAACTG GTTTCCTGCGCATGACTGGGTTCTGCAAAACTAAGATACCTTCTGAGATCACTGCTGCAC

AGATGTGCAAGAAATTCTTGCTACTGGCATTAAGACTTTGCACCTTTACACACTAAACA

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JOURNAL
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AUTHORS
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121 GCTTTATCCGCATGACTGGGTTTTGCAAAACAAAGATACCAGCTGACATTATGGCTGCTT 180
                                                                                                                  702
                                                                                                                                                             61 GCCAAATTGGAATAACGTGTCCTATTGTACCTGGAATTATGCCCCATTAATAATTACAAGG 120
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                                                                                                                                                                                                                                                                                                                                                   1 TGATTGTCACCCAATTATTTTATGATACGGATATATTCCTCAAATTTGTGAACGACTGTC
                                                                                                                  2 (bases 1 to 2225)
Wang, H. and Bohnert, H.
Direct Submission
Submitted (02-AUG-1999) Department of Plant Sciences, University
Arizona, Forbes Building, Room 303, Tucson, AZ 85721, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    higher plants
J. Biol. Chem
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /TITALS LATION-"MKVUEKILEAAGDGRTAFSFEYFPRKTEEGVENLFERMDRMVAH
GPSFCDITWGAGGSTADLTLELANRMONMVCVETMMHLJCTNAFVEKIDHALETIKSN
G1SNULALRGDPHGODK TOVEGFERACALDIVOHIRAKYGDY ETGITVAGYEBAHDA
IQGEGGATLEAYSNDLAYLKRKVDAGADLIVTOLFYDTDIFLKFVNDCRQIGITCPIV
GGIMPINNYKGFLRMTGSFCKTKIDESAVRALDPIKDNEEAVROYGIHLGTEMCKKILA
TGIKTLHLYTLMNDKSAIGILMNLGLIEESKYSRFLFWRATNVFRVKEDVRPFFWAN
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TGIKTLHLYTLMNDKSAIGILMNLGLIEESKYSRFLFWRATNVFRVKEDVRPPFWAN
TGIKTLHYTLMNDKSAIGILMNLGLIEESKYSRFLFWRATNVFRVKEDVRPPFWAN
TGIKTLHYTLMNDKSAIGILMNLGTHRPPKTREDTHRPTTRATNVFRVKEDVRPPKAN
TGIKTLHYTLMNDKSAIGILMNLGTHRPTTRATNVFRVKEDVRPPKGAN
TGIKTLHYTLANNDKSAIGILMNLGTHRPTTRATNVFRVKEDVRPPKROKKEN
TGIKTHLYTLANNDKSAIGILMNLGTHRPTTRATNVFRVKEDVRPPKROKKEN
TGIKTHLYTLANNDKSAIGILMNLGTHRPTTRATNVFRVKEN
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TGIKTHRPTTRATNVFR
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489 c 573 g 587 t
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DSPTVGWGGPGGYVYQKAYLEFFCAKEKLDQLIEKIKAFPSLTYIAVNKDGETFSNIS
PNAVNAVTWGVFPGKEIIQPTVVDHASFMVWKDEAFEIWTRGWGCMFPEGDSSRELLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function="catalyzes the reduction of 5,10-methylenetetrahydrofolate (CH2-THF) 5-methyltetrahydrofolate (CH3-THF)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Zea mays"
/db_xref="taxon:4577"
77. .1858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="methylenetetrahydrofolate reductase"
/protein_id="AAD51733.1"
/db_xref="G1:5802606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="NADH-dependent; MTHFR"
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77.6%;
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                                                                               Louis, MO 631:
On May 4, 2003
Submitted by:
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Caenorhabditis elegans.
Eukaryota, Metazoa, Nematoda,
Rhabditoidea, Rhabditidae, Pel
                                                                                                             Submitted (20-JUL-2002) Department University, Genome Sequencing Cente Louis, MO 63110, USA
                                                                                                                                                                                                            University, Genome St. Louis, MO 63110, USA
                                                                                                                                                                                                                        Submitted (04-MAY-2002) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Ave
                                                                                                                                                                                                                                                                            Waterston, R.
                                                                                                                                                                                                                                                                                        Submitted (07-SEP-2001) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue, Louls, MO 63110, USA 6 (bases 1 to 38571)
                                                                                                                                                                                                                                                                                                                                                                         5 (bases 1 to 38571) Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (10-JUL-2001) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Ave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (01-NOV-1995) Robert Waterston 4 (bases 1 to 38571)
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Direct Submission
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email: rw@nematode.wustl.edu and jes@sanger.ac.uk

NOTICE: This sequence may not be the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between neighboring submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one mil subclone.

For a graphical representation of this cosmid sequence and its analysis see: http://www.wormbase.org/db/seq/sequence?name=C06A8;class=Sequence

# NEIGHBORING COSMID INFORMATION

The 5' cosmid is B0228, 750 bp overlap. Actual start of this cosmid is at base position 1 of C06A8; actual end is at 38570 of C06A8.

### NOTES:

Coding seqences below are the result of integration and manual review of the following data: computer analysis using the program Genefinder (P. Green and L. Hillier, personal communication), the large scale EST projects of Yuji Kohara (http://www.ddbj.nig.ac.jp/c-elegans/html/CE\_INDEX.html) and The C. elegans Orgeome cloning project (http://worfdb.dfci.harvard.edu/), similarity to other proteins from BlastX analyses (http://blast.wustl.edu/), sequence conservation with C. brigsae using Jim Kent's WABA alignment program (Genome Research 10:1115-1125, 2000), individual C. elegans GenBank submissions, and personal communications with C. elegans researchers. trNAs are predicted using the program trNAscan-SE (Lowe, T.M. and Eddy, S.R., 1997, Nucl. Acids. Res., 25, 955-964). /product="Hypothetical protein C06A8.7"
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8874. .8980)) /gene="C06A8.1 /note="coded

for by

the following

C. elegans cDNAs

complement(join(4021. .4083,4508. .4582,4629. .4745, 6304. .6410,6934. .7016,7594. .7619,8511. .8689,8736.

.8827

CDS

gene

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http://www.wormbase.org/db/seq/sequence?name=C06A8.la;clas
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http://www.wormbase.org/db/seq/sequence?name=C06A8.6;class
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Submitted (01-AUG-2002) Horticultural Sciences, University Florida, Hull Road, Gainesville, FL 32611, USA Sequence update by submitter On Aug 1, 2002 this sequence version replaced gi:19550442.
                                                                                                         Submitted (29-OCT-2001) Horticultural Sciences, University of Florida, Hull Road, Gainesville, FL 32611, USA 3 (bases 1 to 1785)
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Roje,S., Raymond,R.K.,
Direct Submission
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                                                                                                                                                               CAAAGGGCTGGAATGACTTCCCACATGGACGTTGGGGTGATTCACACAGTGCAGCATACA 109
                                                                                                                                                                                                                                            AAAACGAGGAAGTCAGACCTATCTTCTGGGCAAACCGTCCAAAGAGCTACATATCTAGAA
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ASLPOPTIDITWINAGGRILSHLSTDLVATAQSVLGLETCMLTCTNMPISMIDDALENA
YHSGCQNILALRGDPPRDAENWTPVEGGFQYAKDLIKYIKSKYGDHFAIGVAGYPECH
PELPINKDVKIDLEFKIKQKIDAGGDFIITQMFYDVDNFINWCSQVRAAGMDPFIIFGIM
PITTYAAFLRRAQWGQISIPQHFSSRLDPIKDDDELVRDIGTNLIVEMCQKLLDSGYV
SHLHIYTMMLEKAPLMILERLNILPTESEFNAHPLAVLPWRSGINFKKNEEVRPIFW
ANRRKSYLSTRTKGWMDEPHGRWGDSHSAMYSTILSDYGARPKGRDKKLLQEWVYPLKS
IEDVQEKFKELCIGNLKSSPWSELDGLQPETKIINEQLGKINSNGFLTINSQPSVNAA
KSDSPAIGWGGPGGYVYQKAYLEFFCSKDKLDTLVEKSKAFPSITYMAVNKSENWYSN
TGESDVNAVTWGVFPAKEVIQPTIVDPASFKVWKDEAFFIWSRSWANLYPEDDPSRKL
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/product="chimeral"
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Pred. No. 8.6e-22;
D; Mismatches 243;
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                                                                                                                                                                                                                                                                                                              TTGGAATAACGTGTCCTATTGTACCTGGAATTATGCCCATTAATAATTACAAGGGCTTTA 126
                                        GTAGACGTCTTCTCGATAACGGATCAGCTCCATCGATTCATTTATATACCATGAATCGTG 7103
                                                                                                                       CAATCAAGCATGATGACGACGCTGTTCAAAAGTATGGAACTGAGCGATGTATTGAAATGT
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                                                                                                                                                                                                      AGCGTATCGCTAAACTCTCCCAACTGGAAATTCCTGAGCACATTCTCGAAGATCTTGAGC 7223
                                                                                                                                                                                                                                            TCCGCATGACTGGGTTTTGCAAAACAAAGATACCAGCTGACATTATGGCTGCTTTAGAGC 186
                                                                                                                                                                                                                                                                                    TCGGAATCACCAAACCAATCATTCCTGGAATCATGCCAATCATGGGATACGAATCCATCA 7283
  AGAAATCTGCATTGGCAATACTAATGAACCTTGGCCTAATTGAAGAGTCCAAAGTTTCTA 363
                                                                                GCAAAAAGATTTTAGCTCATGGAATTAAGACATTG----CATCTTTATACACTAAATATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemist; or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one ml3 subclone.
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Submitted (20-NOV-2001) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Ave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 81624)
Washington University Genome Sequencing Center
The C. briggsae Genome Sequencing Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Waterston, R
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Department of Genetics, Washington University
St. Louis, MO 63110, USA
email: rw@nematode.wustl.edu
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/db_xref="Haxon:6238"
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54.0%;

    Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGAACGGAAGATGGGGAAACAGTTCTTCTCCAGCATTTGGTG 6881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CACATGGGCGTTGGGGTGATTCCTGTAATCCATCATATGGTG 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCTACTGGAGCTTCCGTCCTCGCAGTTATATCACCAGAACTCGCGATTGGGATCAGTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTTTTGGGCAAATCGACCAAAAAGCTACATATCAAGGACCATAGGATGGGATCAATACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGTTCCCATGGAAAAATCGTTCTCAACATCCAATCAGATGTCTTGAAAGTGTTCGCCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGGGAAGCATTCGTGAGATTCTAAAAGCTCTTGGATTGTGGAAGCTCGAAGGAGATCGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
Rosidae; eurosids II; Brassicales; Brassicaceae; Arab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (27-FEB-2002) The Institute for Genomic Research, Submitted (27-FEB-2002) The Institute for Genomi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (09-MAR-2000) The Institute for Genomic Research, Medical Center Dr., Rockville, MD 20850, USA 3 (bases 1 to 109741)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 109741)
Rounsley,S.D., Kaul,S., Lin,X., Ketchum,K.A., Crosby,M.L.,
Brandon,R.C., Sykes,S.M., Mason,T.M., Kerlavage,A.R., Adams,M.D.,
Somerville,C.R. and Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Medical Center Dr. Rockville, MD 20850, USA, co
On Apr 18, 2002 this sequence version replaced
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
2 (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(1. .4149)."
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eudicots;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(<9101. .9952,10049. .10409,10500. .10623, 10717. .10984,11093. .11133,11219. .11384,11587. .11671, 11768. .11895,12004. .12811,12910. .13162,13259. .>14090))
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join(7192 .7632 ~~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FLRNIACTETOLWAGQESGVRFWNFDDAFEPGCGLSGRVQRGDEDAAPFQESASTSPT
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YGDLWSCSEGGVIKIWTWESMEKSLSLRLEEKHMAALLVERSGIDLRAQVTVNGTCNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(join(9101. .9952,10049. .10409,10500. .10623, 10717. .10984,11093. .11133,11219. .11384,11587. .11671, 11768. .11895,12004. .12811,12910. .13162,13259. .14090)), gene="At2943900"
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                                                                                                                                                                                                       CSKSQKKSDGDTNSKSQKKGDGDSSSKSHKKNDGDSSSKSHKKNDGDSSSKSHKKSDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MDIINNNHRDENDDDEEEALSAMSSYPPPRKIHSYSHQLRATGQ
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                                                                                                                                                                                                                                              KSSKKSDGDSNSKSSKKSDGDSNSKSSKKSDGDSNSKSSKKSDGDSNSKSSKKSDGDS
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complement(join(14925. .14963,15285. .15363,15476. .15522, 15617. .15716,15874. .15974,16059. .16145,16677. .16807, 17119. .17218))
/gene="At2g43910"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="At2g43930"
/note="F6E13.6; coi
(PDOC00100)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="AT_rich" complement(19342...21515) /gene="At2g43920"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(16570..16608)
/rpt_family="AT_rich"
complement(17642..17687)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="maeeqqusdosnggnviptpeevatflhktveeggwekcweeei
TPWDQGRATPLIVHLVDTSSLPLGRALVPGCGGGHDVVAMASPEREVVGLDISESALA
KANETYGSSPKAEYFSFVKEDVFTWRPTELFDLIFDXVFFCAIEPEMRPAWAKSMYEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(19586.
20130. .20229,20308.
21416. .21515))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(join(<19342. .19624,19773. .19851,19988. .20034, 20130. .20229,20308. .20408,20521. .20607,20828. .20958,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_family="AT_rich" 18152. .18196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(15108. .15141)
/rpt_family="AT_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="unknown protein"
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17774. .17794
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                                                                                                                                                                           FPEPKHHNRYLLDNAFISHYKSVKNIHQQSFKIEIDPRKEKKQS"
complement(27269. .30414)
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PFFCSLCRNALGHGNVTSEPHIVLLLQCRKKSWCFASEFEHLKLFKGYIDEDEERHKF
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                                                                                     complement(join(<27269. .27361,27641. 28336. .28397,28479. .28537,28635. .2
                                                                                                                                                                                                                                                                                                                                                             /product="putative protein kinase"
/protein_id="AAC23427.1"
/db_xref="GI:3212876"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           join(23418. .23599,24062. .24130,24488.
24898. .25008,25727. .>25849)
/gene="%L2g43930"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="At2g43920"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="F6E13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LKPDGELITLMYPITDHVGGPPYKVDVSTFEEVLVPIGFKAVSVEENPHAIPTRKGKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24898.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="At2g43920"
complement(join(27269. .27361,27641.
                                                                                                                                                     /note="F6E13.7"
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                               /gene="At2g43940"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oin(23455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _fami
                                                            .29343,30043. .>30414))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     155. .23599,24062. .24130,24488.
25008,25727. .25849)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contains a protein kinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . .19851,19988.
.20607,20828. .
                                                                                               .28784,28865.
      .27771,27853. .27984
                                                                                                                           .27771,27853.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .24592,24751.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .20958,
                                                                                                     .28981,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .24812
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SPAC56F8
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AUTHORS
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
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                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93932 G
                                                                                                                                     source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               329 G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Walsh,S.V
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Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93812 TGTGAAAGCCTATGGTATTCACCTTGGAACAGAGATGTGTAAAAAAGATGTTGGCTCATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     149 AACAAAGATACCAGCTGACATTATGGCTGCTTTAGAGCCTATCAAGGACAATGAAGAAGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGTCAAGTCTCTTCATCTCTACACATTGAACATGGAGAAATCTGCTCTTGCAATATTGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AATTAAGACATTGCATCTTTATACACTAAATATGGAGAAATCTGCATTGGCAATACTAAT 328
                                                                                                                                                                                                                       The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

INPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a
                                                                                                                                                                                                                                                                                                                                                                                                 (URL, http://www.sanger.ac.uk/Projects/S_pombe)
Protein coding regions (CDS) have been predicted with the help of
computer analysis using the Genefinder program in PomBase (an ACEDB
database) with additional predictions for the branch-acceptor sites
supplied by the program Sp3splice. CAUTION: It is possible that for
any individual CDS we may have underestimated or overestimated the
number of introns/exons or we may not have chosen the correct
splice donor/acceptor sites.
CDS are numbered using the following system eg SPAC5H10.01c. SP (S.
pombe), A (chromosome 1), c5H10 (cosmid name), .01 (first CDS), c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alpha-glucosidase; escl; methylenetetranydrorolate reductase;
microsomal signal peptidase;
para-hydroxybenzoate--polyprenyltransferase; probable membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPAC56F8 37093 bp
S.pombe chromosome I cosmid c56F8
Z69728
                                                                                                                       small overlap between neighbouring submissions. Cosmid c56FB is overlapped at the 5' end by cosmid c30D11 and the 3' end by cosmid c22A12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (14-FEB-1996) Schizosaccharomyces sequencing project, Sanger Centre, Hinxton FCB10 1RQ E-mail: barrell@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schizosaccharomyces pombe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Details of yeast sequencing at the Sanger Centre the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Fungi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Z69728.1 GI:1204222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schizosaccharomycetales; Schizosaccharomycetaceae
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                                                                                                                                                                                                                                                                                                                                                                                    (complementary strand)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submission
                       /db_xref="taxon:4896"
                                                                          /organism="Schizosaccharomyces pombe"
/chromosome="I"
                                                  /strain="972h-"
                                                                                                       .37093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          esc1; methylenetetrahydrofolate reductase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                    cosmid c30D11 and
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CDS gene

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                                                                                                                                                                                                                                        GELHGVVISHRTILHOMNCLAAIHATAPAYESDKLDYLSIDREYTEGLSKSGLFLTYL
DLRQAIGLILGVLHTVESGYTTVWCPQNAVFVYGLWARLATRY RASFMLTDYAGIKTI
AYNYONDPKATLGFSKKHSVDLSSLRMCMYDCLUVDCEFQEIVSDRWLKPLEKEALKLNEV
TFVPLLCLPEHGGNVISMKDWIGGEEFMSPKGFKSPRTPENEISEVLLEKEALKLNEV
VVLAEDDKARROSKHPWTIRVQAFWYPFVDATLAIVDEETQVLCLPNIYGEIWNDSPS
LSGGFFALFWCOTEALFHARTSFISSDTFOPIDESQEFLRTGLLGFIRKGKYVYVLGLEV
DRLQCKYEWYDNGKQDTIFFHHYTSHLVNTIMRKVSKYFDCSAFDIFVNSEHLPVVLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="SWISS-PROT:Q10250"
/translation="mnQfPnQPGNFGQNYYKPVQGSIPANSEATNFQQNNSRENKSEC
ELRQNSIAASMSAYPNGMYAGAENHNVENHENYTMVGHDHMEEYYGDDLVNEPRIAYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="SPAC56F8.02" len:1517,
/note="SPAC56F8.02, len:1517,
/note="SPAC56F8.02, len:1517,
/note="SPAC56F8.02, len:1517,
/similarity:Schizosaccharomyces pombe, YA84_SCHPO,
hypothetical 162.4 kd protein c22f3.04 in chromosome i.,
hypothetical 162.4 kd protein c22f3.04 in chromosome i.,
(1428_aa), fasta scores: opt: 1491, E():0, (30.0% identity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NSNSNTITCVVSGTMVSSPSLANITILGLSNPPNTILFNGQQLSDYQYSDQTLSLTNL
LDLTVDGAFSKNWTVTWS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTALLISPALEPNTTYIQGIIPGDNDTIWYDWYNHSVINHDYDENITMSAPLGYYNIA
VRGGNIIPLQQPGYTTYESRNNPYSLLIAMDNNGFASGSLYIDDGISMQTNSSLSVKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCGSDLLKLNPVHPPFSLPGDVDNKVYSYPEDFNATNTTEYKSVSRASOSOYKATATS
EKSHETPSSESLINGKPEFSLWPPYALDTDTETHDLAQFGVSPATMIGNTLRYNLF
STYCYSESKISFEALMSIQPNIRPFLLSRSTPYCGSGRYAAHNLGDNKSOSMYSSIS
SILTFNLLGIPMVGADVCGYNGNTDEELCARMMALGAFLPFYRNHNSLGSIPQEPFRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="DLINMRSYLNASNIPTEGFWNDIDYMSEFRTFTVNSTAFPPNQT
LDFFRSLDESHQHYVPVLDPAIYAANPNKSADRTYYPYYSGFEDNIFIKNPNGSAYVG
MAWPGFVVYPDFTNPAVLQYWKQGILNLSTAFGSNYSYDLPFSGLCLDMNEPTSFCIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="putative family glucosidase) precursor" /protein_id="CAA93572.1" /db_xref="GI:1204223"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDRVVLMYRDCEAIDFVVSLFGCFIAGVVAVPINRFDDYNELSSILTTTSARLALTTD
ANLKAFQRDLNAKKLHWPKNVEWWKTNEFGGFHLKKKKAEMPPLQVPDLAYIEFSRSPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pombe
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niger, AGLU_ASPNG, alpha glucosidase precursor, (142)
fasta scores: opt: 1586, E():0, (42.5% identity in 6)
                                                                                                                                      ESPAANIPTEANGNQVVINYGLLDLITTECVECLLEDHQVRVYCVLICAPFTLPRVTK
NGRQEIGNMMCRRAFEHGTLPFLYVKFAVERAVLNLPVGEDAIDGIWSSYASGIRQNL
LSDQELQYSGFIDRSLRYDAKTSVDISSCHTMLQLLQLRVAKNAEDIAYITIDGRGRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FTNIAAVLRYRGVHSAKKTAFIILDNKGKEFTSITWEKLASRAEKVAQVIRDKSGLFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SDIVATFDGKDFGSNLHVDDTLDQQWAHFAGKQQHPLEPREIPFPVTDPLNSKIEMKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="hypothetical integral membrane protein"
/protein_id="CAA93573.1"
/db_xref="GI:1204224"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Match to PF01055 Glyco_hydro_31, Glycosyl
hydrolases family 31 Score 977.93"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASVAEASRSAIEIRYSLLPYWYTLMHTASVDGTPMVRPLFFEFPKQISLASVDKQFMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /partia
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/note="SPAC30D11.01c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
/label=SPAC56F8.02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label=SPAC56F8.01
                                                                   VPPLDHMRLSEDVPAFLFLIKHYYVSAVLVNSEADTALRAKTTSQHLKQSAMAAKVVL
                                                                                                     GKNITWRKFDQRVATIIRYLQKKKYIKPGRVVVLMYTHSEDFVYALYACFYLGLIPIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in 1372 aa)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="SPAC56F8.02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="SPAC56F8.01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="SPAC56F8.01"
/note="nominal overlap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="SWISS-PROT:Q09901"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="SPAC56F8.01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone="cosmid c56F8"
|CQIHKETCQMTHKRPLLGHVRSMSGIGFFHTCLMGVFLGTTTYLLSPVDFANNPLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chromosome 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cosmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               glycosyl hydrolase (alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPAC30D11,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EM: Z67961
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GYVYAGLINGEKY,KYTINEKS, NIBGITSILSSSGLLENSPATSILSVEDPORDSK
DSEKVERETEYERKEENEAERAEVPDDWEAALEEPEYAENNEYTEKKETDIKSDAVE
HSIKDKEDSKTDKVDDIPQAAPAESNVSESDLKSPICCILGHVDIGKTKLLDNLRSN
VQEGEAGGITQOJGATYFPIESIKQKTKVVNKKGKLQYNIPGLLIIDTPGHESETNLR
SRGTSLCNIAILVIDIMHGLEPQTIESIRLRDOKTPFVVALNKVDRLYGWHSIKDNA
IQDSLSKQKKALQREFSDRVESIILQLNEQGLMAALYFENKNLGRYVSLVPTSAQSGE
GVPDLVALLISLTQTRMSDRIKYITTLECTVLEKVLJEGATIDVILSKGVLHEEDR
IVLCGMGGPIITTVRALLTPQPLKEMRVKSAVVHKEIKAAMGVKICANDLEKAVAGS
ILLVVGPDDDEEDLAEEIMEDLENLLGRIDTSGIGVSVQASTLGSLEALLEFLKQMKK
                                                                                                               TYHLFDAFTAHQKKILEQKREESSDVAVFPCVLKTVAAFNKRDPIILGVDVVEGVLRI
NTPIVAVKQLPNGEPQIIELGRVASLEMNHKPVDKVKKGQAGAGVAMKLESSGSQILF
GRQVTESDALYSHITRQSIDSLKDPAFRDEVSRDEWQLIIQLKKLFGII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KPKKGKKGKKSKKVEEDDEPQEIESPQGPKELTAVTELDDDEFDYKPKKGKKGKKAQN
NNESEAAAPPEIPEVRVKTKKEKEREKKEREKLRKKQQQAKKKGSTGEDTLASSEVSS
EVDISTPAENDSSAKGKQAAGSKRKGPNVTALQKMLEEKRAREEEEQRIREEEARIAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MGKKGKKSGYADWEDDLGEDISGQNEYLDNTSQDSPQNDELAEK
SENLAVSSEKTTSKKKKGKKNKGNKNQVSDDESQELESPQGPKELTAVTELDDDEFDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="SPAC56F8.03, len:1079, SIMILARITY:Saccharomyces cerevisiae, IF2P_YEAST, translation initiation factor if-2., (1002 aa), fasta scores: opt: 3165, E():0, (52.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DYNPSLRSTPSVSSRSTLPQRVF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NATNSDGFLGNGYVRTGDLGFLQITSHSMGPNAPVVDMQLLYVLGPIGETFEVNGLSH
FPSDIEDTIERSHPRIARGGTAVFQSAGRVVVVIEALGQDFLAAIVPVVINSILDEHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FQIISKYKIKDTYATFQTLNYIQNQQPTKWPNLSCLENLMIPHDGRISAFYIASLQKY
FVKHGLSPYAFSTVYSNCLNPFISTRSYMGAIPTPQLLDLRALRHGLIQPCESADKPY
ALPLLDSGMVPVSTQLAIVNPDTRELCRVGEYGEIWMRSSANAISFFQSTDPVDMMRF
                                                                                  8488.
                                                                                                                                                                                                                                               PVASVNIGPVYKKDVMRCATMLEKAKEYALMLCFDVKVDRDAEDLAEQLGVKIFSANV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EEKRLAEVEEARKEEARLKKKEKERKKKEEMKAQGKYLSKKQKEQQALAQRRLQQMLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="translation initiation
/protein_id="CAA93574.1"
/db_xref="GI:1204225"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="SPAC5
7948. .11187
    /gene="SPAC56F8.03"
/note="Match to PF00992 Troponin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   identity in 1015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IIADVVAFTSRGNFPRSRLREKQRGKILASWVTGRLRTTQVFYIRGSGEGEFQSSYVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="SWISS-PROT:Q10251"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label=SPAC56F8.03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="SPAC56F8.03"
note="Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   factor if-2"
    Troponin Score 22.61"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E():0, (52.8%
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misc\_feature misc\_feature /product="para-hydroxybenzoate--polyprenyltransferase, mitochondrial precursor(ec 2.5.1.-)"
/protein\_id="CaNa9575.1"
/db\_xref="GI:1204226"
/db\_xref="GI:1204226"
/db\_xref="SMISS-PROT:010252"
/dasref="SMISS-PROT:010252"
PNLISPSKKSWKDLFSKRWQYYAEISRAGSPTGTYLLYSPCTWSILMAAYAYDSSIVN
VTKMLALFGVGSFLMRSAGCVINDLWDRELDAKVERSKSRPLASGKLSVROAISLLSV E():0, (48.3% identity in 296 aa)" /codon start=1 complement(11653. para-hydroxybenzoate--polyprenyltransferase, mitochondrial
precursor(ec\_2.5.1.-), (372\_aa), fasta scores: opt: 909, cerevisiae, COQ2\_YEAST, /gene="SPAC56F8.04c" /note="SPAC56F8.04c" /note="PS00017 ATP/GTP-binding complement(11626. .12702) SNTGYLVAAAIALDWLAKSFIYDS" CGLAALQIATLATAGIMNGQGPVFYTLGVAGAAYRLSSMIYKVDLDDPKDCFRWFKRN QLTASLGILLQLNPYTIKLGVASLVPVCIYPAMKRITYYPQVVLGLTFGYGAVMGWPA /codon\_start=1 /label=SPAC56F8.04c LAGEACMNWSVVAPLYLSTTSWIVLYDTIYAHQDKRDDVKANIYSTALRFGDNTKPVL /note="SPAC56F8.04c, len:358, SIMILARITY:Saccharomyces /gene="SPAC56F8.04c" /gene="SPAC56F8.03" site motif

/note="Match to PF01040 COX10\_ctaB\_cyoE,
oxidase assembly factor Score 444.71"

Cytochrome c

/gene="SPAC56F8.04c" /note="Match to PF01

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RESULT 14
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AX069359
                                                                                                          Detection of analytes using attenuated enzymes Patent: WO 0102600-A 23 11-JAN-2001; GENERAL ATOMICS (US)
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14129...14176,14332...14370,14511...14570))
/gene="SPACSGF8.05C"
complement(join(13097...13461,13595...13802,13917.
                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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Johnson,W.G. and Stenroos,E.Scott.
Methods for diagnosing, preventing, and treating development disorders due to a combination of genetic and environmental Patent: US 6219950-A 1 03-APR-2001;
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Search completed: February 14, 2003, 21:20:23 Job time: 3017 secs

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                        98US-0092869
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nilarity 79.9%;
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Query Match 62.0%;
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QY 45 TTTGTGAACGACTGTCGCCAAATTGGAATAACGTGTCCTATTGTACCTGGAATTATGCCC 104

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misc_feature
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                                          14-JUL-1999;
                                                                      27-JAN-2000
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                15-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                          99WO-US15916
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74..107
/*tag=
                                                                                                                           /note= "corresponds
positions 25-26 of 1
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/transl_except= (pos:120..122.aa:Xaa)
/transl_except= (pos:174..176.aa:Xaa)
/note= "Xaa= unknown"
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/product= "5,10-methylenetetrahydrofolate
/product= "1.7.99.5"
                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                           two unknown amino acids (Xaas) at corresponding protein sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is a cDNA clone wlm96.pk047.14 encoding 5,10-methylenetetrahydrofolate reductase (MTHFR). The clone was isolated from a wlm96 cDNA library which was prepared using wheat seedlings obtained 96 hrs. after inoculation with E. graminis. WTHFR plays a role in the synthesis of methionine.

The present sequence is used in the construction of a chimeric gene to after the level of tetrahydrofolate metabolism enzymes in plants. The enzyme may provide target to facilitate design and/or identification of inhibitors that may be useful as herbicides. The polynacleotide is also useful as a source of probes for genetically and physically mapping the genes and as markers for traits linked to the genes.
                                                                                             Human; schizophrenia; developmental disorder; spina bifida cyst
Tourette's syndrome; bipolar illness; autism; conduct disorder;
attention deficit disorder; obsessive compulsive disorder;
chronic multiple tic syndrome; learning disorder; polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 451 BP; 135 A; 89 C; 101 G; 117 T; 9 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Pages 34-35; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel tetrahydrofolate metabolism enzyme used to alter the level of tetrahydrofolate metabolism in plants and seeds \, -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Falco
                                          WO200071754-A1
                                                                      Homo
                                                                                                                                                                    Human methylenetetrahydrofolate reductase gene SEQ ID
                                                                                                                                                                                                  20-MAR-2001
                                                                                                                                                                                                                            AAC91206;
                                                                                                                                                                                                                                                      AAC91206 standard;
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DB; AAY44741.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCTTTATCCGCATGACTGGGTTTTTGCAAAACAAAGATACCAGCTGACATTATGGCTG-CT
                                                                     sapiens.
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                                                                                                                                                                                                                                                                                                                            TGAAGATGTTCAAAAAAATTTTNGGCTAGTGGGATAAANACNTTGCA 450
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213; Conserv
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Pred. No. 1.8
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                                                                                               polymorphism; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides a novel method of estimating the susceptibility of an individual to a developmental disorder using genetic and environmental variables. The method can be used in the diagnosis, prevention and treatment of disorders such as schizophrenia, spina bifida cystica, Tourette's syndrome, bipolar illness, autism, conduct disorders, attention deficit disorder, obsessive computative disorder, chronic multiple tic syndrome and learning disorders such as dyslexia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Diagnosing a developmental disorder, e.g. schizophrenia, by forming datasets (DS) of genetic (e.g. genotypes of folate metabolism alieles) and environmental variables affecting an individual and then comparing these DS with reference DS -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 114-115; 156pp; English.
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                                                                     ACTACCTCTT
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                                                                                                                                                                                                                                                                                                                                                                           TTTCTAGGTCCTTACCTTGGAGACGCCCTGCAAATGTTTTCCGTGTTAAAGAAGATGTCC 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCCTGTGCCAGGAGCTTCTGGCCAGTGGCCTGGTGCCAGGCCTCCACTTCTACACCCTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAGAGCCTATCAAGGACAATGAAGAAGCTGTCAAGGCTTATGGAATTCACCTGGGAACTG
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                                                                                                                  ATCAGTTCAT
                                                                                                                                                                                                                                                     GTCCCATCTTCTGGGCCTCCAGACCAAAGAGTTACATCTACCGTACCCAGGAGTGGGACG
                                                                                                                                                                                                                                                                                                                                             ACCGCGAGATGGCTACCACAGAGGTGCTGAAGCGCCTGGGGGATGTGGACTGAGGACCCCA 1033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATATGGAGAAATCTGCATTGGCAATACTAATGAACCTTGGCCTAATTGAAGAGTCCAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTGAGCCAATCAAAGACAACGATGCTGCCATCCGCAACTATGGCATCGAGCTGGCCGTGA 913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCCTTCGGCAGCTTGTGAAGCTGTCCAAGCTGGAGGTGCCACAGGAGATCAAGGACGTGA 853
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                                                                                                                                                          AGTTCCCTAACGGCCGCTGGGGCAATTCCTCTTCCCCTGCCTTTGGGGAGCTGAAGGACT
                                                                                                                                                                                                  AATACCCACATGGGGGTGGGTGATTCCTGTAATCCATCATATGGTGCATTATCTGATT 537
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AC AAT09689;
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AC AAT09689;
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Human methylene-tetr
DE Human methylene-tetr
PE Human methylene tetrahydro
KW Methylene-tetrahydro
KW Cardiovascular disea
KW EC-1.5.1.20; enzyme;
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HOMO saplens.
FH Key 13.
FH Key 13.
FT CDS 13.
XX
W09533054-A1.
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PD 07-DEC-1995.
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PN W09533054-A1.
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PT 25-MAY-1995; 95WO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence encoding human MTHFR has been localised to chromosome 1936.3. It may be used for the construction of DNA probes which may be used for the identification of sequence abnormalities in patients with severe or mild MTHFR deficiency. The resulting probe may also be used in gene therapy to produce the MTHFR protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human methylene:tetra:hydro:folate reductase cDNA probe - for detection of sequence abnormalities in methylene:tetra:hydro:folate reductase e.g. in cardiovascular, neurological or folic acid metabolism disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2219 BP; 501 A; 656 C; 620 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig.6A-6C; 66pp; English.
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                                          AAATGTGCAAAAAGATTTTAGCTCATGGAATTAAGACAT----TGCATCTTTATACACTAA
                                                                                                                                                                                                  CCCTTCGGCAGCTTGTGAAGCTGTCCAAGCTGGAGGTGCCACAGGAGCATCAAGGACGTGA
                                                                                                                                     TAGAGCCTATCAAGGACAATGAAGAAGCTGTCAAGGCTTATGGAATTCACCTGGGAACTG
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DB; AAR88358.
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Pred. No. 2.
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The invention relates to a non allele-specific antisense nucleic acids, which binds to methylenetetrahydrofolate reductase (MTHFR; EC 1.5.1.20) nucleic acids and inhibits MTHFR protein expression in a mammal. MTHFR catalyses the NADPH-linked reduction of 5,10-methylenetetrahydrofolate 5-methylenetetrahydrofolate, a co-substrate for methylation of
                                                                                                Disclosure;
                                                                                                                                          New antisense nucleic acids, which are methyleneretrahydrofolate reductase inhibitors, useful for treating, stabilizing or preventing cancer, e.g. breast carcinoma, colon carcinoma, colorectal carcinoma
                                                                                                                                                                                                         WPI; 2001-638509/73.
P-PSDB; AAE12607.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; methylenetetrahydrofolate reductase; MTHFR; gene therapy; glioma; antisense therapy; EC 1.5.1.20; chromosome 1p36.3; cancer; kidney cell; pancreas; lung; brain; cytostatic; colon carcinoma; breast; colorectal; neuroblastoma; leukaemia; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human methylenetetrahydrofolate reductase (MTHFR) protein cDNA
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SEKHON J.
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/product= "Human methylenetetrahydrofolate
(MTHFR) protein"
/EC_number= "1.5.1.20"
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                                                Methylene-tetrahydrofolate-reductase; MTHFR; gene therapy; cardiovascular disease; neurological disease; folic acid m EC-1.5.1.20; enzyme; ss.
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                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCGACATGGGCATCACTTGCCCCATCGTCCCCGGGATCTTTCCCATCCAGGGCTACCACT
                                                                                                                                                                                                                                                                                                                      ATCAGTTCAT
                                                                                                                                                                                                                                                                                                                                                                                  AATACCCACATGGGCGTTGGGGTGATTCCTGTAATCCATCATATGGTGCATTATCTGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCGCGAGATGGCTACCACAGAGGTGCTGAAGCGCCTGGGGATGTGGACTGAGGACCCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCTGTGCCAGGAGCTTCTGGCCAGTGGCTTGGTGCCAGGCCTCCACTTCTACACCCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAATGTGCAAAAAGATTTTAGCTCATGGAATTAAGACAT---TGCATCTTTATACACTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTGAGCCAATCAAAGACAACGATGCTGCCATCCGCAACTATGGCATCGAGCTGGCCGTGA
                                                                                                                                                                                                                                                                                                                                                      AGTTCCCTAACGGCCGCTGGGGCAATTCCTCTTCCCCCTGCCTTTGGGGAGCTGAAGGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             293;
                                                                                                               methylene-tetrahydrofolate-reductase cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                             standard; cDNA;
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Pred. No. 2.6e
0; Mismatches
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6e
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1042

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1219 537 1159 922

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metabolism;

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Query Match
Best Local S:
Matches 293
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mat_peptide
                                                                                            1100
                                                                                                                                                                              1040
       1160 AGTTCCCTAACGGCCGCTGGGGCAATTCCTCTTCCCCTGCCTTTGGGGAGCTGAAGGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence encoding human MTHFR has been localised to chromosome 1936.3. It may be used for the construction of DNA probes which may be used for the identification of sequence abnormalities in patients with severe or mild MTHFR deficiency. The resulting probe may also be used in gene therapy to produce the MTHFR protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human methylene:tetra:hydro:folate reductase cDNA probe - for detection of sequence abnormalities in methylene:tetra:hydro:folate reductase e.g. in cardiovascular, neurological or folic acid metabolism disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2220 BP; 501 A; 657 C; 620 G; 442 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig.1A-1F; 66pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goyette P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-DEC-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GCCAAATTGGAATAACGTGTCCTATTGTACCTGGAATTATGCCCCATTAATAATTACAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 53.3 es 293; Conservative
                                  GTCCAATCTTTTGGGCAAATCGACCAAAAAGCTACATATCAAGGACCATAGGATGGGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAGAGCCTATCAAGGACAATGAAGAAGCTGTCAAGGCTTATGGAATTCACCTGGGAACTG
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;DB; AAT09694.
                                                                                                                                                                            CCAGGCGTCCCTACCCTGGGCTCTCAGTGCCCCACCCCCAAGCGCCGAGAGGAAGATGTAC
                                                                                                                                                                                                                                                                                                                                                                            AAATGTGCAAAAAGATTTTAGCTCATGGAATTAAGACAT---TGCATCTTTATACACTAA
                                                                                                                                                                                                                                                                                                                                                                                                                              TTGAGCCAATCAAAGACAACGATGCTGCCATCCGCAACTATGGCATCGAGCTGGCCGTGA
                                                                                         GTCCCATCTTCTGGGCCTCCAGACCAAAGAGTTACATCTACCGTACCCAGGAGTGGGACG
                                                                                                                                                                                                       TTTCTAGGTCCTTACCTTGGAGACGCCCTGCAAATGTTTTCCGTGTTAAAGAAGATGTCC
                                                                                                                                                                                                                                                                                                                                                GCCTGTGCCAGGAGCTTCTGGCCAGTGGCTTGGTGCCAGGCCTCCACTTCTACACCCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCTTCGGCAGCTTGTGAAGCTGTCCAAGCTGGAGGTGCCACAGGAGATCAAGGACGTGA
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                                                                                                                                                                                                                                                                                         ATATGGAGAAATCTGCATTGGCAATACTAATGAACCTTGGCCTAATTGAAGAGTCCAAAG
                                                                                                                                                                                                                                                              ACCGCGAGATGGCTACCACAGAGGTGCTGAAGCGCCTGGGGATGTGGACTGAG---GATC
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/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English.
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RESULT 11
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                                          CDNA probe for the human methylenetetrahydrofolate reductase (WHHFR), useful in gene therapy and for dispnosing or treating WHHFR deficiency which is associated with cardiovascular disorders or cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Methyleneterrahydrofolate reductase; MPHFR; human; cardiovascular disorder; cancer; neuroblastoma; colorectal carcinoma; osteopporosis; neural tube de;
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    Claim 1; Fig 1A-F; 93pp; English
                                                                                                                                                                                             Rozen
                                                                                                                                 P-PSDB;
                                                                                                                                                                                                                                                                                  01-MAR-1999;
                                                                                                                                                                                                                                                                                                                       28-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                    08-SEP-2000.
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                                                                                                                               2000-572192/53.
DB; AAY96186.
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                                                                                                                                                                                                                                     UNIV MCGILL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard; cDNA; 2220
                                                                                                                                                                                           Goyette P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ar disorder; cancer; neuroblastoma;
arcinoma; osteoporosis; neural tube defect;
disorder; gene therapy; diagnosis; chromosome
                                                                                                                                                                                                                                                                                                                          2000WO-IB00442
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                                                                                                                                                                                                                                                                             9908-0258928
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/*tag= j
replace(1018,T)
/*tag= k
/*tag= k
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/*tag= h
replace(985,T)
/*tag= i
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  replace(1317,C)
/*tag= m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          replace(1298,C)
/*tag= 1
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/*tag= f
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/*tag= e
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/*tag= d
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/*tag= c
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/*tag= g
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/*tag= b
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13..1983
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The present sequence is that of cDNA coding for human CC methylenetetrahydrofolate reduction of 5,10-methylenetetrahydrofolate catalysing the NADPH-linked reduction of 5,10-methylentrahydrofolate CC to 5-methyletrahydrofolate, a co-substrate for methylation of CC homocysteine to methionine. To identify human MMHFR cDNA, PCR primers based on the porcine sequence were used to screen a human CC liver lambda-gt10 cDNA library by PCR. A 1266 bp fragment was obtained, and this was used to screen a human colon carcinoma cDNA CC library to obtain the 2.2 kb clone. The MMHFR gene (see AAA50634) CC maps to chromosome 1p36.6. A cDNA probe for human MMHFR, which hybridises to the present sequence, is claimed. This probe can be CC used to identify MMHFR sequence abnormalities in individuals with severe or mild MMHFR deficiency. These abnormalities may comprise CC a mutation selected from 167c to A, 482G to A, 550c to T, 677C to T, 692C to T, 764C to T, 792+1G to A, 985C to T, 1015C to T, 1081C CC to T, 1298A to C and 131T to C. MMHFR peficiency may be associated CC with a cardiovascular disorder, cancer (especially neuroblastoma or Cc colorectal carcinoma), osteoporosis, neural tube defect in an offspring of a patient, neurological disorders, and other disorders for CC treating MMHFR peficiency by gene therapy or by administration of CC expression or MMHFR protein activity, or by administering an agent that modifies MMHFR gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
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                                                                                                                                                                                                                                                            GTCCAATCTTTTGGGCAAATCGACCAAAAAGCTACATATCAAGGACCATAGGATTGGGATC
                                                                                                                                                                                                                                                                                                                                                                                                                 TTTCTAGGTCCTTACCTTGGAGACGCCCTGCAAATGTTTTCCGTGTTAAAGAAGATGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATATGGAGAAATCTGCATTGGCAATACTAATGAACCTTGGCCTAATTGAAGAGTCCAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAATGTGCAAAAAGATTTTAGCTCATGGAATTAAGACAT---TGCATCTTTATACACTAA 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTGAGCCAATCAAAGACAACGATGCTGCCATCCGCAACTATGGCATCGAGCTGGCCGTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCGACATGGGCATCACTTGCCCCATCGTCCCCGGGATCTTTCCCATCCAGGGCTACCACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCATCATCACGCAGCTTTTCTTTGAGGCTGACACATTCTTCCGCTTTGTGAAGGCATGCA 742
ATCAGTTCAT 547
                                                                                                                   AATACCCACATGGGCGTTGGGGTGATTCCTGTAATCCATATATGGTGCATTATCTGATT
                                                                                                                                                                                                                       GTCCCATCTTCTGGGCCTCCAGACCAAAGAGTTACATCTACCGTACCCAGGAGTGGGACG
                                                                                                                                                                                                                                                                                                                                                                   ACCGCGAGATGGCTACCACAGAGGTGCTGAAGCGCCTGGGGGATGTGGACTGAGGACCCCA 1042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCTTTATCCGCATGACTGGGTTTTGCAAAACAAAGATACCAGCTGACATTATGGCTGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 53.3
93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 116.4; DB 21; Length Pred. No. 2.5e-24; 0; Mismatches 251; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G; 441 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6;
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                                                                                                                                            537
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Query Match Best Local Matches

Similarity

20.9%;

Score 116.4; Pred. No. 2.6e 0; Mismatches

6e-24 DB 22;

2220; 6;

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Sequence 2220 BP; 501 A; 658

C; 620 G; 441 T; 0 other;

B

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DЬ Qy Db Q DP

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The invention relates to a non allele-specific antisense nucleic acids, which binds to methylenetetrahydrofolate reductase (MTHFR; EC 1.5.1.20) nucleic acids and inhibits wTHFR protein expression in a mammal MTHFR catalyses the NADPH-linked reduction of 5.10-methylenetetrahydrofolate, a co-substrate for methylation of homocysteine to methionine. The invention provides potential therapy for individuals with MTHFR deficiency. The non allele-specific antisense nucleic acids are useful for treating, stabilising or preventing cancer, particularly breast carcinoma, colon-carcinoma, colorectal carcinoma, lung cancer, brain cancer, pancreatic cancer, kidney cell cancer, neuroblastoma, gloma and leukaemia. MTHFR cDNA probe is used in gene therapy. The present sequence is human methylenetetrahydrofolate reductase (MTHFR) protein cDNA #1. Human MTHFR gene is mapped to chromosome 1p36.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; methylenetetrahydrofolate reductase; MTHFR; gene therapy; glioma; antisense therapy; EC 1.5.1.20; chromosome 1p36.3; cancer; kidney cell; pancreas; lung; brain; cytostatic; colon carcinoma; breast; colorectal; neuroblastoma; leukaemia; ss.
                                                                                                                                                                                                                                                                                                       New antisense nucleic acids, which are methylenetetrahydrofolate reductase inhibitors, useful for treating, stabilizing or preventing cancer, e.g. breast carcinoma, colon carcinoma, colorectal carcinoma neuroblastoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAD20462 standard; cDNA; 2220
                                                                                                                                                                                                                                                                           Disclosure; Fig 1; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US2001025030-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human methylenetetrahydrofolate reductase (MTHFR) protein cDNA #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                        2001-638509/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ROZEN R.
SEKHON J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0728910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1..1983
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a
/product= "Human methylenetetrahydrofolate reductase
/product="CDF does not include start codon"
/EC_number= "1.5.1.20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /partial
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RESULT 13
ABK13501
ID ABK13
XX
AC ABK13
AC ABK13
AX
DT 09-AP
XX Methy
KW Methy
KW neuro
KW antic
KW antic
KW cance
KW nigra
KW cance
KW chron
OS Homo
AX
FT CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                           neuroprotective; tranquiliser; nootropic; antidepressant; anticonvulsant; cerebroprotective; amyotrophic lateral sclerosis; anxiety; dementia; depression; epitepsy; Huntington's disease; migraine; demyelinating disease; multiple sclerosis; pain; Parkinson's disease; psychosis; stroke; cardiovascular disorder; cancer; osteoporosis; metabolic disease; endocrine disease; huborn error of metabolism; inflammation; immune disorder; neuroblastoma; colorectal carcinoma; neophastic disease; renal dichromosome 1p36; ss; EC number 1.5.1.20.
                               12-JUN-2001; 2001WO-CA00867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Methylenetetrahydrofolate reductase; MTHFR; neuroleptic; neuroprotective; tranquiliser; nootropic; antidepressant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding human methylenetetrahydrofolate reductase (MTHFR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-APR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           803 CCCTTCGGCAGCTTGTGAAGCTGTCCAAGCTGGAGGTGCCACAGGAGATCAAGGACGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCTTTATCCGCATGACTGGGTTTTGCAAAACAAAGATACCAGCTGACATTATGGCTGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATCAGTTCAT 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATACCCACATGGGCGTTGGGGTGATTCCTGTAATCCATCATATGGTGCATTATCTGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTCCCATCTTCTGGGCCTCCAGACCAAAGAGTTACATCTACCGTACCCAGGAGTGGGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGCGTC---CCCTACCCTGGGCTCTCAGTGCCCACCCCAAGCGCCGAGAGGAAGATGTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATATGGAGAAATCTGCATTGGCAATACTAATGAACCTTGGCCTAATTGAAGAGTCCAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAATGTGCAAAAAGATTTTAGCTCATGGAATTAAGACAT---TGCATCTTTATACACTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTGAGCCAATCAAAGACAACGATGCTGCCATCCGCAACTATGGCATCGAGCTGGCCGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTACCTCTT 1229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGTTCCCTAACGGCCGCTGGGGCAATTCCTCTTCCCCTGCCTTTGGGGAGCTGAAGGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTCCAATCTTTTGGGCAAATCGACCAAAAAGCTACATATCAAGGACCATAGGATGGGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTTCTAGGTCCTTACCTTGGAGACGCCCTGCAAATGTTTTCCGTGTTAAAGAAGATGTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                  /product= "MTHER"
/note= "Meth-"
                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                            "Methylenetetrahydrofolate reductase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        renal disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CC rhe invention describes a method of diagnosing a psychosis in a subject, CC or a risk for or propensity to psychosis in a subject comprising CC determining the presence of a heterozygous methylenetetrahydrofolate CC reductase (MTHFR) mutant allele in a nucleic acid sample obtained from a CC subject. The method is useful for diagnosing subjects at risk of, or CC suffering from a psychosis, particularly schizophrenia but includes CC manic-depressive disease, organic psychosic disorders, psychosis in CC alcohol or drug intoxication, postinfection psychosis, postpartum CC psychosis, senile psychosis, traumatic psychosis and acute idiopathic CC psychotic illnesses. A new pharmaceutical composition is used for CC treating amyotrophic lateral sclerosis, anxiety, dementia, depression, CC epilepsy, Huntington's disease, migraine, demyelinating disease, multiple CC sclerosis, pain, Parkinson's disease, schizophrenia, psychoses, or CC stroke. Deficiency may be associated with diseases including CC cardiovascular disorders, cancer (e.g. neuroblastoma and colorectal CC cardiovascular disorders, inflammation, immune disorders, neoplastic disease and CC renal disease. This sequence encodes human methylenetetrahydrofolate CC described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local :
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                                                                                        1043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2220 BP; 501 A; 658 C; 620 G; 441 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-130741/17.
P-PSDB; AAU75413.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGATTGTCACCCAATTATTTTATGATACGGATATATTCCTCAAATTTGTGAACGACTGTC 60
                        GTCCAATCTTTTGGGCAAATCGACCAAAAAGCTACATATCAAGGACCATAGGATGGGATC
                                                                                    GGCGTC---CCCTACCCTGGGCTCTCAGTGCCCACCCCAAGCGCCGAGAGAAGAAGATGTAC
                                                                                                                                                                                                                                                   ATATGGAGAAATCTGCATTGGCAATACTAATGAACCTTGGCCTAATTGAAGAGTCCAAAG
                                                                                                                                                                                                                                                                                                                                                                        AAATGTGCAAAAAGATTTTAGCTCATGGAATTTAAGACAT ----TGCATCTTTATACACTAA 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAGAGCCTATCAAGGACAATGAAGAAGCTGTCAAGGCTTATGGAATTCACCTGGGAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCTTTATCCGCATGACTGGGTTTTGCAAAACAAAGATACCAGCTGACATTATGGCTGCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCATCATCACGCAGCTTTTCTTTGAGGCTGACACATTCTTCCGCTTTGTGAAGGCATGCA 742
                                                                                                                                                TTTCTAGGTCCTTACCTTGGAGACGCCCTGCAAATGTTTTCCGTGTTAAAGAAGATGTCC
                                                                                                                                                                                                            ACCGCGAGATGGCTACCACAGAGGTGCTGAAGCGCCTGGGGGATGTGGACTGAGGACCCCA 1042
                                                                                                                                                                                                                                                                                                                                 GCCTGTGCCAGGAGCTTCTGGCCAGTGGCTTGGTGCCAGGCCTCCACTTCTACACCCTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCCTTCGGCAGCTTGTGAAGCTGTCCAAGCTGGAGGTGCCACAGGAGATCAAGGACGTGA
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293; Conserv
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Pred. No. 2.6e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 24; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                251; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2220;
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RESULT 14
ABK13539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Methylenetetrahydrofolate reductase; MTHFR; neuroleptic; neuroprotective; tranquiliser; nootropic; antidepressant; anticonvulsant; cerebroprotective; amyotrophic lateral sclerosis anxiety; dementia; depression; epilepsy; Huntington's disease; migraine; demyelinating disease; multiple sclerosis; pain; Parkinson's disease; psychosis; stroke; cardiovascular disorder; cancer; osteoporosis; methabolic disease; endocrine disease; niborn error of metabolism; inflammation; immune disorder; human
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The invention describes a method of diagnosing a psychosis in a subject, or a risk for or propensity to psychosis in a subject comprising determining the presence of a heterozygous methylenetetrahydrofolate reductase (MTHFR) mutant allele in a nucleic acid sample obtained from a subject. The method is useful for diagnosing subjects at risk of, or suffering from a psychosis, particularly schizophrenia but includes manic-depressive disease, organic psychotic disorders, psychosis in alcohol or drug intoxication, postinfection psychosis, postpartum
                                                                                                                                                                                                 Diagnosing subjects at risk for or suffering from a psychosis, particularly schizophrenia comprises determining the presence of heterozygous methylenetetrahydrofolate reductase mutant allele in
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                                                                                                                                                                                    subject
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                                                                                                                                                                                                                                                                                                                      Rozen
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DB; AAU75421.
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1.5.1.20; mutant.
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/note= "Methylenetetrahydrofolate reductase"
replace(167,6)
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     Human methylenetetrahydrofolate reductase (MTHFR) G482A allele
                                       09-APR-2002
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standard;

cDNA; 2220

ВP

(first entry)

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             psychosis, senile psychosis, traumatic psychosis and acute idiopathic psychotic illnesses. A new pharmaceutical composition is used for treating amyotrophic lateral sclerosis, anxiety, dementia, depression, epilepsy, Huntington's disease, migraine, demyelinating disease, multi sclerosis, pain, parkinson's disease, schizophrenia, psychoses, or stroke. Deficiency may be associated with diseases including cardiovascular disorders, cancer (e.g. neuroblastoma and colorectal carcinoma), osteoporosis, metabolic or endocrine disease, inborn error of metabolism, inflammation, immune disorders, neoplastic disease and renal disease. This sequence encodes a mutant human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       methylenetetrahydrofolate reductase (MTHFR, EC number nucleotide 167 has been altered to produce a mutant the method of the invention.

Note: This sequence does not appear in the specification of the wild type sequence (ABK13501) using created from the wild type sequence (ABK13501)
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ACTACCTCTT 1229
                                          ATCAGTTCAT
                                                                                     AGTTCCCTAACGGCCGCTGGGGCAATTCCTCTTCCCCTGCCTTTGGGGGAGCTGAAGGACT
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a mutant allele, described
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The invention describes a method of diagnosing a psychosis in a subject, CC or a risk for or propensity to psychosis in a subject comprising CC determining the presence of a heterozygous methylenetetrahydrofolate creductase (MTHFR) mutant allele in a nucleic acid sample obtained from a CC subject. The method is useful for diagnosing subjects at risk of, or CC suffering from a psychosis, particularly schizophrenia but includes CC manic depressive disease, organic psychotic disorders, psychosis in CC alcohol or drug intoxication, postinfection psychosis, postpartum cCC psychosis, senile psychosis, traumatic psychosis and acute idiopathic CC psychosis, senile psychosis, traumatic psychosis and acute idiopathic CC psychotic illnesses. A new pharmaceutical composition is used for CC creating amyotrophic lateral sclerosis, anxiety, dementia, depression, cc psychosis, pain, parkinson's disease, schizophrenia, psychoses, or CC stroke. Deficiency may be associated with diseases including CC cardiovascular disorders, cancer (e.g. neuroblastoma and colorectal CC cardiovascular disorders, schoolate reductase (MTHFR, EC number 1.5.1.20), in which CC created from the wild type sequence (ABK13501) using information given the nethod of the invention.
Query Match
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P-PSDB; AAU75422.
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued\_Patents\_NA:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

970 357	911 GCCTGTGCCAGGAGCTTCTGGCCAGTGGCTGGTGCCAGGCCTCCACTTCTACACCTCA 298 ATATGGAGAAATCTGATTGGCAATACTAATGAACCTTGGCCTAATTGAAGAGTCCAAAG 1
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CTG	QY 181 TAGAGCCTATCAAGGACAATGAAGAAGCTGTCAAGGCTTATGGAATTCACCTGGGAACTG 240
TT 180	Qy 121 GCTTTATCCGCATGACTGGGTTTTGCAAAACAAAGATACCAGCTGACATTATGGCTGCTT 180
G 6	Qy 61 GCCAAATIGGAATAACGTGTCCTATTGTACCTGGAATTATGCCCATTAATAATACAAGG 120
IC CA	Oy 1 TGATTGTCACCCAATTATTTATGATACGGATATATTCCTCAAATTTGTGAACGACTGTC 60
Gaps	Query Match 20.9%; Score 116.4; DB 4; Length 1971; Best Local Similarity 53.3%; Pred. No. 2e-27; Matches 293; Conservative 0; Mismatches 251; Indels 6;
Ħ	; ORGANISM: Homo sapiens ; FEATURE: ; FEATURE: ; OTHER INFORMATION: Human methylenetetrahydrofolate reductase (MTHFR) ; OTHER INFORMATION: gene: exons 1-8 ; PUBLICATION INFORMATION: ; DATABASE ACCESSION NUMBER: AF105977/GenBank 1-11 US-09-347-878-23
	: SOFTWARE: PatentIn Ver. 2.0 ; SEQ ID NO 23 ; LENGTH: 1971 ; TYPE: DNA
U)	US-09-347-678-23 ; Sequence 23, Application US/09347878C ; Patent No. 6376210 ; GENERAL INFORMATION: ; APPLICARY: Yuan, Chong ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES ; FILE REFERENCE: 25865-1651 ; CURRENT APPLICATION NUMBER: US/09/347,878C ; CURRENT SILING DATE: 1999-07-06 ; NUMBER OF SEQ ID NOS: 75
	RESULT 1

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APPLICANT: Johnson, William G.
APPLICANT: Stenzoos, Edward S.
APPLICANT: Stenzoos, Edward S.
ITTLE OF INVENTION: METHODS FOR DIAGNOSING, PREVENTING, AND TREATING TITLE OF INVENTION: DEVELOPMENTAL DISORDERS
FILE REFERENCE: 601-1-057
CURRENT APPLICATION NUMBER: U5/09/318,448
CURRENT FILING DATE: 199-05-25
NUMBER OF SEQ ID NOS: 46
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 2187
TYPE: DNA
ORGANIZM: Homo sapiens
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--- rocal Similarity
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1091 GTCCCATCTTCTGGGCCTCCAGACCAAAGAGTTACATCTACCGTACCCAGGAGTGGGACG 1150
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0; Mismatches 251;
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AFFLANCE CHASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION UNMBER: WO PCT/CA95/00314

FILING DATE: 25-MAY-1995

PRIOR APPLICATION UNMBER: GB 9410620.0

FILING DATE: 26-MAY-1994

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2219 base pairs

TORNE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: CDS
; LOCATION: 13..1983
US-08-738-000-3
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                                                                                                                                                                                                                                                                              Best Local Similarity 53.3 Matches 293; Conservative
                                                                                                                                                                                                                                                                                                Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/08738000 Patent No. 6074821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: KLAUBER & JACKSON
ATREET: Continental Plaza - 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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   863
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ZIP: 07601
                                                                                                                                                                                                                                1 TGATTGTCACCCAATTATTTATGATACGGATATATTCCTCAAATTTGTGAACGACTGTC 60
APPACCACAPTGGGGTTGGGGTGATTCCTCTAATCATATATGGGAGAGCTGAATGATT 537
AATACCACAPTGGGGGTTGGGGTGATTCCTCTAATCATATGGGGAGCTGAAGCACT 121
AGTTCCCTAACGGCGCTGGGGCAATTCCTCCTTCCCCTGCCTTTGGGGAGCTGAAGGACT 121
                                                                                                                                                               GCCAAATTGGAATAACGTGTCCTATTGTACCTGGAATTATGCCCCATTAATAATTACAAGG 120
                                                                   CCCTTCGGCAGCTTGTGAAGCTGTCCAAGCTGGAGGTGCCACAGGAGATCAAGGACGTGA 862
                                                                                                     GCTTTATCCGCATGACTGGGTTTTGCAAAACAAAGATACCAGCTGACATTATGGCTGCTT 180
                                                                                                                                       CCGACATGGGCATCACTTGCCCCATCGTCCCCGGGATCTTTCCCATCCAGGGCTACCACT 802
                                                                                                                                                                                                           TCATCATCACGCAGCTTTTCTTTGAGGCTGACACATTCTTCCGCTTTGTGAAGGCATGCA 742
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                                                                                                                                                                                                                                                                            Score 116.4; DB 3; Pred. No. 2.1e-27; 0; Mismatches 251;
                                                                                                                                                                                                                                                                                                              Length 2219;
                                                                                                                                                                                                                                                                              Indels
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Sequence 3, Application US/09258928

Patent No. 6218120

GENERAL IMPOWADION:
APPLICANT: ROZEN RIMB

APPLICANT: ROZEN, Philippe
ITITLE OF INVENTION: CDNA FOR HUMAN METHYLENETETRAHYDROFOLATE
ITITLE OF INVENTION: REDUCTASE
ITITLE OF INVENTION: REDUCTASE
CURRENT APPLICATION UNMBER: US/09/258,928

CURRENT FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: 089738,000
PRIOR FILING DATE: 1997-02-12
PRIOR APPLICATION NUMBER: 089410620.0
PRIOR FILING DATE: 1994-05-26

PRIOR FILING DATE: 1994-05-26

NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 2219
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US-09-258-928-3
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; LOCATION: (13)...(1983)
US-09-258-928-3
                                                                                                                                                                                                                                                                                                                           Query Match 20.9
Best Local Similarity 53.3
Matches 293; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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                          181 TAGAGCCTATCAAGGACAATGAAGAAGCTGTCAAGGCTTTATGGAATTCACCTGGGAACTG
                                                                                                             121 GCTTTATCCGCATGACTGGGTTTTGCAAAACAAAGATACCAGCTGACATTATGGCTGCTT 180
                                                                                                                                                              743 CCGACATGGGCATCACTTGCCCCATCGTCCCCGGGATCTTTCCCCATCCAGGGCTACCACT
                                                                                803 CCCTTCGGCAGCTTGTGAAGCTGTCCAAGCTGGAGGTGCCACAGGAGATCAAGGACGTGA
                                                                                                                                                                                      61 GCCAAATTGGAATAACGTGTCCTATTGTACCTGGAATTATGCCCATTAATAATTACAAGG 120
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TTGAGCCAATCAAAGACAACGATGCTGCCATCCGCAACTATGGCATCGAGCTGGCCGTGA 922
                                                                                                                                                                                                                                                                                                                         20.9%; Score 116.4; DB 4; Length 2219; 53.3%; Pred. No. 2.1e-27; ative 0; Mismatches 251; Indels 6;
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MESULT 5
US-08-738-000-1
Sequence 1, Application US/08738000
Patent No. 6074821
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                                                                                ; NAME/KEY:
; LOCATION:
US-08-738-000-1
                                                                                                                                                                                                                                              CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UNMBER: WO PCT
FILING DATE: 25-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION UNMBER: GB 941
APPLICATION UNMBER: GB 941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2220 base pairs
Query Match
Best Local Similarity 53.3
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: doub!
TOPOLOGY: linear
MOLECULE TYPE: DNA (9:
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1160
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                                                                                                                                  ANTI-SENSE:
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            358
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                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: Continen
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: KLAUBER & JACKSON
STREET: Continental Plaza - 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTCCAATCTTTTGGGCAAATCGACCAAAAAGCTACATATCAAGGACCATAGGATGGGATC
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                                                                                                                                                                                     DNA (genomic)
                                                                                                                                                                                                                  double
                             20.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA FOR HUMAN METHYLENETETRAHYDROFOLATE
                                                                                                                                                                                                                                                                                                                                                                        WO PCT/CA95/00314
                                                                                                                                                                                                                                                                                                                         GB 9410620.0
             0;
             Score 116.4; DB 3; Pred. No. 2.1e-27; 0; Mismatches 251;
                                             Length
                                                   2220;
                 6,
               Gaps
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GENERAL INFORMATION:
APPLICANT: ROZEN, Rima
APPLICANT: ROZEN, Philippe
APPLICANT: ROZEN, Philippe
TITLE OF INVENTION: CDNA FOR HUMAN METHYLENETETRAHYDROFOLATE
TITLE OF INVENTION: REDUCTASE
CURRENT APPLICATION NUMBER: US/09/258,928
CURRENT APPLICATION NUMBER: US/09/258,928
CURRENT FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: 08/738,000
PRIOR FILING DATE: 1997-02-12
PRIOR FILING DATE: 1997-02-12
PRIOR APPLICATION NUMBER: GB 9410620.0
PRIOR FILING DATE: 1994-05-26
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 1
SEQ ID NO 1
LENGTH: 2220
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US-09-258-928-1
                                                                                                                                     ; NAME/KEY: CDS
; LOCATION: (1)...(1980)
US-09-258-928-1
                                                                     Query Match
Best Local s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09258928 Patent No. 6218120
                                              Query Match 20.9%;
Best Local Similarity 53.3%;
Matches 293; Conservative
                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                              TYPE: DNA
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  1 TGATTGTCACCCAATTATTTATGATACGGATATATTCCTCAAATTTGTGAACGACTGTC 60
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                                           Score 116.4; DB 4;
Pred. No. 2.1e-27;
0; Mismatches 251;
                                              Indels
                                                                                    Length 2220;
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; Sequence 140, Application US/08961527; Patent No. 6420135; GENERAL IMPORMATION;
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                                                                                                      FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                         SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
NAME: Brookes, A. Anders REGISTRATION NUMBER: 36,373 REFERENCE/DOCKET NUMBER: PB: TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1220 ACTACCTCTT 1229
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ADDRESSEE: Human Gen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                418 GTCCAATCTTTTGGGCAAATCGACCAAAAAGCTACATATCAAGGACCATAGGATGGGATC 477
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US-08-961-527-140
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Best Local Similarity 47.8%;
Matches 150; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 54, Application US/08858207A Patent No. 6348328 GENERAL INFORMATION:
APPLICANT: Black, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hodgson, John
APPLICANT: Knowles, David
APPLICANT: Nicholas, Richard
APPLICANT: Stodola, Robert
TITLE OF INVENTION: No. 6348328el Compounds
NUMBER OF SEQUENCES: 552
CORRESPONDENCE ADDRESS:
ADDRESSEE: Smithkline Beecham Corporation
STREET: 709 Swedeland Road
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INFORMATION FOR SEQ ID NO: 140:
                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 19406-0939
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
MEDIUM TYPE: IBM Compatible
The Compatible
The Compatible
   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/017670
FILING DATE: 14-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRAFION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P50475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15801 TCGTAACTCAGCTCTTTCTTTGACAATGAGCGCTTCTATGATTTTCAGGACAAGTGTATCT 15742
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LENGTH: 28882 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
SOFTWARE: FASTSEQ FOR WINDOWS VERSION 2.0
CURRENT APPLICATION NUMBER: US/08/858,207A
FILING DATE: 09-MAY-1997
CIACTETING ON 4AE-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 TAGAGCCTATCAAGGACAATGAAGGAGCTGTCAAGGCTTATGGAATTCACCTGGGAACTG 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 709 Swedeland CITY: King of Prussia STATE: PA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
US-08-286-630-3/c
; Sequence 3, Application US/08288630
; Patent No. 5837848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC COMPUTER: 126
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: PSTEME: PC-DOS/MS-DOS
SOFTWARE: PSTEME: PC-DOS/MS-DOS
SOFTWARE: PSTEME: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION UNMEER: US/08/288,630
FILING DATE: 10-AUG-1994
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMEER: US 08/111,590
FILING DATE: 25-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION UNMEER: US 07/669,433
FILING DATE: 15-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 7.0%; Score 38.8; DB 4; Best Local Similarity 47.5%; Pred. No. 0.0093; Matches 149; Conservative 0; Mismatches 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATE APPLICANT: F
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LENGTH: 1449 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.
STREET: 1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1171 ATGCTGATACAGCA 1184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1051 TAGACAAGTATGAGCATGACCCTGAGTCGCTCAGAGCAGCAGGACTTGCCTATGCAGTGG 1110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          991 CTCTCCGACTCTTGAAGACTTGTGAGAATATCCATCTTCCACGCAAATTTAAAGCCATCT 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 TTATCCG---CATGACTGGGTTTTGCAAAACAAAGATACCAGCTGACATTATGGCTGCTT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 931 TGGCTGGGATTGATGTTCCCCATTCATGCAGGAATTATGCCAATTCTGAATCGAAATCAGG 990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     871 TCGTAACTCAGCTCTTTGACAATGAGCGCTTCTATGATTTTCAGGACAAGTGTATTT 930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 AAATTGGAATAACGTGTCCTATTGTACCTGGAATTATGCCCATTAATAATTACAAGGGCT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 TIGICACCCAATTATTTTAIGATACGGATATATTCCTCAAATTTGTGAACGACTGTCGCC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LICANT: ELY, SUSAN
LICANT: EVANS, IAN J
LICANT: SCHUCH, WOLFGANG
LE OF TOWNSTION: ROOT-SPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAGAGCCTATCAAGGACAATGAAGAAGCTGTCAAGGCTTATGGAATTCACCTGGGAACTG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGAGAAATCTGCA 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCAANICGTGGACTTGGTAACTCAGGATGTTGCCGGTGTGCATCTCTATACGATGAATA 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAATGTGCAAAAAGATTTTAGCTCATGGAATTAAGACATTGCATCTTTATACACTAAATA 300
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20005-3918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D.C.
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linear
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ROOT-SPECIFIC PROMOTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54:
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RESULT 10
US-09-221-017B-931
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US-08-288-630-3
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REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 2159
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEPAX: (202) 822-094
TELEPAX: (202) 822-094
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4203 base pairs
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COUNTYER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COmpatible
OPERATING SYSTEM: Windows
SOFTWARE: PRESTEM: Windows
SOFTWARE: PRESTEM: US/09/221/0178
APPLICATION NUMBER: US/09/221/0178
FILING DATE: 3-DEC-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION NUMBER: PP1546
FILING DATE: 30-DATA:
APPLICATION NUMBER: PP2911
APPLICATION UNMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION UNMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION UMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION UMBER: PCT/AU98/01023
FILING DATE: 10-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 931, Application US/09221017B Patent No. 6444799
GENERAL INFORMATION:
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Best Local Similarity 50.3%;
Matches 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: ROSS, BRUCE C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF NUMBER OF SEQUENCES: 1120
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION: NAME: KOKULIS, PAUL, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: /22 | STREET: /22 | CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9006017.9
FILING DATE: 16-MAR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 ATACCAGCTGACATTATGGCTGCTTTAGAGCCTATCAAGGACAATGAAGAAGCTGTCAAG 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 510 TCATAGTAATTTCATAGGAGTGGAATGGAGTGATATACTTTGTAGAAACTAAT 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   276 ACATTGCATCTTTATACACTAAATATGGAGAAATCTGCATTGGCAATACTAAT 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              570 AGTTATGTCTTACTGCTAAGCAAGCGAAGGAGGAAGATGACCTCGATTGAAATTAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    216 GCTTATGGAATTCACCTGGGAACTGAAATGTGCAAAAAGATTTTAGCTCATGGAATTAAG 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           630 ATGTCAGGTGATTAGATTTTTGTTCAAATTAAAAGGCAAACTATTGAGCAAGGTAAAGGA 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
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pred. No. 0.19;
0; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     215964/SEE35669USCIP
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                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: RATO, IKUNOSHIN
TITLE OF INVENTION: DUA POLYMERASE-RELATED FACTORS
FILE REFERENCE: 1422-408PCT
COURRENT APPLICATION NUMBER: US/09/446,504
COURRENT APPLICATION NUMBER: PCT/JP98/02845
PRIOR APPLICATION NUMBER: PCT/JP98/02845
PRIOR APPLICATION NUMBER: JP 9-187496
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1997-06-26
PRIOR FILING DATE: 1997-06-26
PRIOR FILING DATE: 1997-07-232692
PRIOR FILING DATE: 1997-11-27
NUMBER: JP 9-320692
PRIOR FILING DATE: 1997-11-27
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US-09-446-504-41
                                                    ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-09-446-504-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-221-017B-931
                                                                                                                                                                                                                                    SOFTWARE: Pares SEQ ID NO 41
LENGTH: 989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -09-4--
Sequence 41, Approx
Sequence 41, S
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Best Local Similarity 50.3%;
Matches 78; Conservative
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Best Local S
                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 92
SOFTWARE: Patentin Ver. 2.1
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TELEX: 706141
INPORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 3152 base pairs
                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3034 CACAAACGGCTGATTTTCTTGCACAAAAACATTTT 3068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2974 GAGATTCTTCCCGATAGACAGCGTTCCAATGACCTTGCTGCAAAAGTAAGGAAGATAATC 3033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2914 AATGTTAACCATTATTGTTTTGTCCGGAATACTTTGTTTTTCCCCCGAAAAGGATCCGCA 2973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Monroy, Gladys H
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   165 GACATTATGGCTGCTTTAGAGCCTATCAAGGACAATGAAGAAGCTGTCAAGGCTTATGGA 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                225 ATTCACCTGGGAACTGAAATGTGCAAAAAGATTTT 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature LOCATION: 1...3152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: PORYPHYROMONAS GINGIVALIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: doub
TOPOLOGY: circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MUKAI, Hiroyuki
ASADA, Kiyozo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIYAKE, Kazue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/09446504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UNKNOWN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     double
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27
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RESULT 12
US-09-712-266-41
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CURRENT FILING DATE: 2000-11-15
PRIOR APPLICATION NUMBER: US 09/446,504
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: PCT/JP98/02845
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: JP 9-187496
PRIOR APPLICATION NUMBER: JP 9-187496
PRIOR APPLICATION NUMBER: JP 9-320692
PRIOR APPLICATION NUMBER: JP 9-320692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 41, Application US/09712266 Patent No. 6333158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            Matches
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APPLICANT: MIYAKE, Kazue
APPLICANT: MUKAI, Hiroyuki
APPLICANT: MUKAI, Hiroyuki
APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: DNA POLYMERASE-RELATED FACTORS
FILE REFERENCE: 1422-408PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: UEMORI, Takash
APPLICANT: SATO, Yoshimi
APPLICANT: EUJITA, Tomok
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 1997-11-27
NUMBER OF SEQ ID NOS: 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
381 CGCCCTGCAAATGTTTTCCGTGTTAAAGAAGATG
                                                                                                                                                                                                             261 GCTCATGGAATTAAGACATTGCATCTTTATACACTAAATATGGAGAAAATCTGCATTGGCA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    928 GAACTTTCAAGCGAAGAACTGACTAAAATAGAGG 961
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     868 TTATAATTTAATTTGGGGATAACAATGGATATTGAGGTTCTCAGAAGATTATTGGAGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         321 ATACTAATGAACCTIGGCCTAATTGAAGAGTCCAAAGTTTCTAGGTCCTTACCTTGGAGA 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               808 GATGAAGGAAGACTTACATTCCTACTGGCTCCAAGAGTTGAAGAGTGACTTTTCTTTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           261 GCTCATGGAATTAAGACATTGCATCTTTATACACTAAATATGGAGAAATCTGCATTGGCA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  201 GAAGAAGCTGTCAAGGCTTATGGAATTCACCTGGGAACTGAAAATGTGCAAAAAGATTTTA 260
                                                                                                                                                                                                                                                                                   748 GATGAAGTTACAATAAAGTTTGGAAATGAAATGCCCATGCAAATGGAGTATTACATTAGA 807
                                                                                                                                                                                                                                                                                                                                     201 GAAGAAGCTGTCAAGGCTTATGGAATTCACCTGGGAACTGAAATGTGCAAAAAGATTTTA 260
                                                                                                                          321 ATACTAATGAACCTTGGCCTAATTGAAGAGTCCAAAGTTTCTAGGTCCTTACCTTGGAGA 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 5.7%;
Local Similarity 46.7%;
                                                                                                                                                                                                                                                                                                                                                                                    Match 5.7%;
Local Similarity 46.7%;
les 100; Conservative
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                                                                                                                                                                               GATGAAGGAAGACTTACATTCCTACTGGCTCCAAGAGTTGAAGAGTGACTTTTCTTTTCC 867
                                                                           TTATAATTTAATTTGGGGGATAACAATGGATATTGAGGTTCTCAGAAGATTATTGGAGAGA
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                                                                                                                                                                                                                                                                                                                                                                                    Score 31.6; DB 4; pred. No. 1.5; 0; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 989;
                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                 Sequence 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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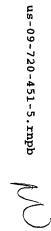
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RESULT 14
US-08-238-163-3/c
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US-08-752-760A-1/c
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GENERAL INFORMATION:
APPLICANY: BENNETT, Alan
APPLICANY: BENNETT, Alan
APPLICANT: LABAVITCH, John M.
APPLICANT: STOTZ, Henrik
TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL
TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: USE FILING DATE: 20-WOV-1S CLASSIFICATION: 435
PRIOR APPLICATION DATA: APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 35081 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: A3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-705-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Seide, Rochelle K
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PastSEO Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Baker & Botts, L.L.P
STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Smith, A TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                               1815 AAATCAAGGCTGTGGAGTACCCTTTCCTGGAAAAGGGACTGGTGGCCGAGATTCAGAGAA 1756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Armentano,
                                                                                                                                                                                                                                                                                                        226 TTCACCTGGGAACTGAAATGTGCCAAAAAGATTTT 259
                                                                                                                                                                                                                                                                                                                                                                                                   166 ACATTATGGCTGCTTTAGAGCCTATCAAGGACAATGAAGAAGCTGTCAAGGCTTATGGAA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U
ZIP: 10112
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STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 5.7%; Local Similarity 58.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 212-705-5020
                                                                                                                                                                                                                                                                                   TCTAGCAGGCCAGAGCAATCAGCAAAAAGATTTT 1722
                                                                                                                                                                                                                                                                                                                                                                                                                                            55;
                                                                                                                                                              , Application US/08238163 5569830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gregory, RICHALL SMITH, Alan E.
SMITH, Alan E.
SMITH, CHIMERIC ADENOVIRAL VECTORS
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Pred. No. 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 35081;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza

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Sequence 13, Application US/09592891A
Patent NO. 6339174
GENERAL INFORMATION:
APPLICANT: Xiao-Zhou Michelle Wang
APPLICANT: Xiao-Zhou Michelle Wang
APPLICANT: Xavier Georges Sarda
APPLICANT: Vincent Paul Mary Wingate
TIFLE OF INVENTION: Heliothis Glutamate Receptor
FILE REFERENCE: A32815 072667.0118
CURRENT APPLICATION UNMEER: US/09/592,891A
CURRENT FILING DATE: 2001-01-22
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; LOCATION:
US-08-238-163-3
                                                                                                                                                                                                                                        RESULT 15
US-09-592-891A-13/c
                                                                                                                                                                                                                                                                                                                                Дb
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TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2075 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 111
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CDREENT APPLICATION DATA:
APPLICATION NUMBER: US/08/238,163
FILLING DATE: 03-MAY-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 2307E-540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                               160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 TTTATCCGCATGACTGGGTTTTGCAAAACAAAGATACCAGCTGACATTATGGCTGCTTTA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local 111;
                                                                                                                                                                                                                                                                                                                                                                     363 AGGT 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                      303 GAGAAATCTGCATTGGCAATACTAATGAACCTTGGCCTAATTGAAGAGTCCAAAGTTTCT 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 GAGCCTATCAAGGACAATGAAGAAGCTGTCAAGGCTTATGGAATTCACCTGGGAACTGAA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     340 TATTTTAGCAATACGGATTTTTGGTCAAGAAAACTGCCCCACAAGTCACTAGTCACATG 281
                                                                                                                                                                                                                                                                                                                              100 AAGT
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                               AATTGATTATAAAATAAAAGGATACTAAAATGAAAATGTTTTTAAAAATGTTAAGTGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGTGCAAAAAGATTTTAGCTCATGGAATTAAGACATTGCATCTTTATACACTAAATATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGTCCAATGATTTTACAATTTATTAATCATGATGTTTATATTCATAGATATTTAATTA 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sinilarity 45.58; Score 31.2; DB 1; Length 2075; Similarity 45.58; Pred, No. 2.9; Indels 0.11; Conservative 0; Mismatches 133; Indels 0.
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, NAME/KEY: unsure
; LOCATION: (764)...(764)
; OTHER INFORMATION: n is a, t,
US-09-592-891A-13
Search completed: February 12, Job time: 132 secs
                                                                                                          20
                                                                                                                                                                                                                                                                                                Query Match 5.6%;
Best Local Similarity 51.9%;
Matches 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 13
LENGTH: 4621
TYPE: DNA
ORGANISM: Heliothis virescens
                                                                                                                                              1981 TTGAGGACTTTATAAGTGCCGAATAAAAGTTCTGCTGTTTAGATGACCAATCAAAATTGA 1922
                                                                       1921 GTCTATTTTTACCGT 1907
                                                                                                                                                                                                                           301 TGGAGAAATCTGCATTGGCAATACTAATGAACCTTGGCCTAATTGAAGAGTCCAAAGTTT 360
                                                                                                                                                                                                                                                241 AAATGTGCAAAAAAGATTTTAGCTCATGGAATTAAGACATTGCATCTTTATACACTAAATA 300
                                                                                                            361 CTAGGTCCTTACCTT 375
                    2003, 15:12:59
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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Published_Applications_NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*

6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*

7: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*

13: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*

14: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*

14: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
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558
1 tgattgtcacccaattattt.....tcagttcatgcggccacgtg 558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Resul'	No.	Score	Query Match	Query Match Length DB	DΒ	ID	Description
1	1	358.8	64.3	1994	9	US-10-113-852A-3	j
	N	273.4	49.0	574	10	US-09-734-017A-61	
	ω	124.4	22.3	264	10	US-09-923-876-5596	
	4	116.4	20.9	2219	9	US-09-931-795-3	
	ഗ	116.4	20.9	2219	10	US-09-728-910-3	
	σ	116.4	20.9	2220	9	US-09-931-795-1	
	7	116.4	20.9	2220	10	US-09-728-910-1	
	œ	112.6	20.2	181	10	US-09-923-876-5753	53
	9	97	17.4	159	10	US-09-294-093B-4653	653
	10	85.6	15.3	409	10	US-09-734-017A-63	w
	11	67	12.0	3082	9	US-10-113-852A-1	
	12	53.4	9.6	640681	10	US-09-790-988-1	
O	13	40	7.2	127197	9	US-09-754-853A-1	
	14	34.8	6.2	1266	10	US-09-815-242-7047	7
o	15	33.4	6.0	2000	9	US-09-938-842A-4584	4
	16	33,2	5.9	6449	9	US-09-938-842A-69	
	17	32.8	5.9	368004	10	US-09-949-654-3	
a	18	32	5.7	1678	10	US-09-764-855-221	
a	19	32	5.7	1680	10	US-09-764-855-220	

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5.4	5.4	5.4	5.4	٠ ت	5.5	5.5	5.5	ნ	5.5	5.5	5 5	5.5	5.6	5.6	5.6	5.6	5. 6	5.6	5.6	5.6	5.6	5.7	5.7	5.7	ارز
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US-09-764-855-173	US-09-938-842A-4582	US-09-938-842A-3505	US-09-938-842A-2860	US-09-764-877-2370	US-09-815-242-8570	US-09-815-242-4642	US-09-938-842A-4958	US-09-774-639-24	US-09-878-574-3994	US-09-878-574-494	US-10-135-322-13	US-09-738-363-5	US-09-969-844-13	US-09-938-842A-4888	US-09-070-927A-307	US-09-796-692-7553	US-09-864-761-2837	US-09-864-761-19619	US-09-796-692-7808	US-09-764-887-35	US-09-783-590-8600	US-09-782-378A-26	US-09-971-309-41	US-09-864-761-16164	US-09-759-508B-1
Sequence 173, App	Sequence 4582, Ap	Sequence 3505, Ap	Sequence 2860, Ap	Sequence 2370, Ap	Sequence 8570, Ap		Sequence 4958, Ap	Sequence 24, Appl	Sequence 3994, Ap	Sequence 494, App	Sequence 13, Appl	Sequence 5, Appli	Seguence 13, Appl	Sequence 4888, Ap	Sequence 307, App	Sequence 7553, Ap	Sequence 2837, Ap	Sequence 19619, A	Sequence 7808, Ap	Sequence 35, Appl	Sequence 8600, Ap	Sequence 26, Appl	Sequence 41, Appl	Sequence 16164, A	Sequence 1, Appli

# ALIGNMENTS

Ф	Qy	ф	Qy	Вb	VΩ	M B s	2	US-1			٠.	••	٠.	٠.	; SI	.,	, .						;	; ,	  . G	79		TIS-1	222
748 GGTTCTTGCGTATGGCTGGTTTCTGTAAGACCAAGATACCCGCTGAGCTCACTGCCTGC	121	688 GCAAATCGGGATTAATTGTCCCATTGTTCCTGGAATTATGCCTATTTCCAACTACAAGG 747	61 GCCAAATTGGAATAACGTGTCCTATTGTACCTGGAATTATGCCCATTAA	> 628 TGATTGTGACTCAGCTTTTCTATGATACTGATATATTCCTCAAGTTTGTGAATGATGATTGTC 687	1	Best Local Similarity 78.0%; Pred. No. 4.1e-94; Best Local Similarity 78.0%; Pred. No. 4.1e-94; Indels 0; Gaps 0; Matches 432; Conservative 0; Mismatches 122; Indels 0; Gaps 0;	54 38.	ÚS-10-113-852A-3	OTHER INFORMATION: DNA CONSTRUCT	NAME/KRY: CUS	FEATURE	ORGANISM: Arabidopsis thaliana	TYPE: DNA	LENGTH: 1994	SEQ ID NO 3	SOFTWARE: PatentIn version 3.0	NUMBER OF SEQ ID NOS: 13	PRIOR FILING DATE: 2001-03-30	PRIOR APPLICATION NUMBER: 60/280,333	CURRENT FILING DATE: 2002-03-29	CTREES ADELT TARTOA ATTABES IS (10 /10 /113 R52)	TITLE OF INVENTION: BIOSYNTHESIS OF S-AGENOSYL METHIONINE IN a RECOMMINANT YEAST STEE PROFESSION 110037-1032			GENERAL INFORMATION: APPLICANT: Appling, Dean R.	Publication No. US20020192784A1	Sequence 3, Application US/10113852A	TS-10-713-852A-3	COTTO 1

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: TYPE: DNA
: ORGANISM: Physcomitrella patens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)..(573)
: OTHER INFORMATION: 86_PPprot1_094_g10
US-09-734-017A-61
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US-09-734-017A-61
                                                                                                                                                                                                                                                                                                                                        APPLICANT: Freund, Annette
APPLICANT: Duwenig, Elke
APPLICANT: Schmidt, Ralf-Michael
TITLE OF INVENTION: Moss genes from Physcomitrella patens encoding proteins involved
TITLE OF INVENTION: Synthesis of amino acids, vitamins, cofactors, nucleotides and
TITLE OF INVENTION: DIVERSION: Synthesis of amino acids, vitamins, cofactors, nucleotides and
TITLE OF INVENTION: nucleosides
FILE REFERENCE: BASF-NAE-131-99-US
CURRENT APPLICATION NUMBER: US/97/734,017A
CURRENT FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: 60/171,100
PRIOR FILING DATE: 1999-12-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 61, Application US/09734017A Patent No. US20020142422A1 GENERAL INFORMATION:
                                                                                                 Matches
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APPLICANT:
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                              1 TGATTGTCACCCAATTATTTTATGATACGGATATATTCCTCAAATTTTGTGAACGACTGTC 60
     8 TCATTATCACCCAGCTGTTTTATGATACCGATATCTTTTTGAAATTTGTGAATGATTGTC
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                                                                                                                   Similarity
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Ehrhardt, Thomas
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                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jens
                                                                                                                49.0%; Score 273.4; DB 10; 69.7%; Pred. No. 1.2e-69;
                                                                                              Mismatches
                                                                                            166;
                                                                                                                                       Length
                                                                                                                                       574;
                                                                                         Gaps
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                                                                                         μ;
                                                                                                                                                                                                                                                                                                                                                     Sequence 5596, Application US/09923876
Patent No. US20020013958A1
GENERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
FILE REFERENCE: PL-0012-1 CON
CURRENT APPLICATION NUMBER: US/09/923,876
CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 09/298,329
PRIOR FILING DATE: 1999-04-21
PRIOR FILING DATE: 1999-05-05
NUMBER OF SEQ ID NOS: 6332
SOFTWARE: PERL Program
SEQ ID NO 5596
S
                                                                                                                                     ; OTHER INFORMATION: a, t, c, g, or other US-09-923-876-5596
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US-09-923-876-5596
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                                           Query Match
Best Local Similarity
Matches 166; Conserv
                                                                                                                                                                              ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20020013958A1 700457310H1
NAME/KEY: unsure
LOCATION: 81, 183
                                                                                                                                                                                                                                                                                                                      LENGTH: 26
TYPE: DNA
340 TAATTGAAGAGTCCAAAGTTTCTAGGTCCTTACCTTGGAGACGCCCTGCAAATGTTTTCC 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTAGGTCCTTACCTTGGAGACGCCCTGCAAATGTTTTCCGTGTTAAAGAAGATGTCCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGAGAAATCTGCATTGGCAATACTAATGAACCTTGGCCTAATTGAAGAGTCCAAAGTTT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCCAAATTGGAATAACGTGTCCTATTGTACCTGGAATTATGCCCATTAATAATTACAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAATCTTTTGGGCAAATCGACCAAAAAGCTACATATCAAGGACCATAGGATGGGATCAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAATGTGCAAAAAGATTTTAGCTCATGGAATTAAGACATTGCATCTTTATACACTAAATA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAGAGCCTATCAAGGACAATGAAGAAGCTGTCAAGGCTTATGGAATTCACCTGGGAACTG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTTTCTCCGCATGACCACCTTGTGCAAGACCAAGGTGCCAGCTGAAATCATGGCTGCAC 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTCAAATTGGTATCAAGGTGCCCATTGTACCTGGTATCATGCCCCATTCAAAATTACAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTATTTTCTGGGCCAACCGACCTAGAAGCTACATTTCACGAACCACCAGCTGGGACGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTCGTCCTCTACCGTGGAGGCCTCCAACTAACAGCAAGCGTACAAAGGAGGACGTGCGTC
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                                                                                                                                                                                                                                                                                                                                             264
                                              Conservative
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                                                                22.3%;
                                         ; Score 124.4; 1; Pred. No. 1.2e 0; Mismatches
                                           ..2e-26;
tes 53;
                                                                                       DB 10;
                                              Indels
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Sequence 3, Application US/09931795
; Sequence 3, Application US/09931795
; Publication No. US20020198211A1
; GENERAL IMFORMATION:
TITLE OF INVENTION: CDNA FOR HUMAN METHYLENETETRAHYDROFOLATE
TITLE OF INVENTION: REDUCTASE AND USES THERBOF
; FILE REFERENCE: 04844/005003
; CURRENT APPLICATION NUMBER: US/09/931,795
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: US 09/592,595
; PRIOR FILING DATE: 1999-03-01
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: US 09/258,928
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: US 08/738,000
; PRIOR APPLICATION NUMBER: US 08/738,000
; PRIOR FILING DATE: 1997-02-12
; PRIOR APPLICATION NUMBER: US 08/738,000
; PRIOR FILING DATE: 1998-03-05
; PRIOR FILING DATE: 1998-05-25
; PRIOR FILING DATE: 1998-05-25
; PRIOR FILING DATE: 1994-05-26
; PRIOR FILING DATE: 1998-05-27
; PRIOR FILING DATE: 1998-05-25
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US-09-931-795-3
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; LOCATION: (13)...(1983)
US-09-931-795-3
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124
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                                                                                                                                                                      863 TTGAGCCAATCAAAGACAACGATGCTGCCATCCGCAACTATGGCATCGAGCTGGCCGTGA 922
                                                                                                                                                                                                                            181 TAGAGCCTATCAAGGACAATGAAGAAGCTGTCAAGGCTTATGGAATTCACCTGGGAACTG 240
                                                                                                                                                                                                                                                                                      803 CCCTTCGGCAGCTTGTGAAGCTGTCCAAGCTGGAGGTGCCACAGGAGATCAAGGACGTGA 862
                                                                                                                                                                                                                                                                                                                           121 GCTTTATCCGCATGACTGGGTTTTGCAAAACAAAGATACCAGCTGACATTATGGCTGCTT 180
                                                                                                                                                                                                                                                                                                                                                                                                          743 CCGACATGGGCATCACTTGCCCCCATCGTCCCCGGGATCTTTCCCATCCAGGGCTACCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          583 TCATCATCACGCAGCTTTTCTTTGAGGCTGACACATTCTTCCGCTTTGTGAAGGCATGCA 742
298 ATATGGAGAAATCTGCATTGGCAATACTAATGAACCTTGGCCTAATTGAAGAGTCCAAAG 357
                                                      923 GCCTGTGCCAGGAGCTTCTGGCCAGTGGCTTGGTGCCAGGCCTCCACTTCTACACCCTCA 982
                                                                                                         241 AAATGTGCAAAAAGATTTTAGCTCATGGAATTAAGACAT---TGCATCTTTATACACTAA 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TGATTGTCACCCAATTATTTTATGATACGGATATATTCCTCAAATTTGTGAACGACTGTC 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GIGITAAAGAGGATGTINCGACCIATATICTGGGCCAACAGACCAAAGAGCTATCTTAAA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTGTTAAAGAAGATG-TCCGTCCAATCTTTTGGGCAAATCGACCAAAAAGCTACATATCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             293;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20.9%; Score 116.4; DB 9; ilarity 53.3%; Pred. No. 5.9e-24; Conservative 0; Mismatches 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2219;
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RESULT 5
US-09-728-910-3
US-09-728-910-3
Sequence 3, Application US/09728910
Patent No. US20010025030A1
GENERAL INFORMATION:
APPLICANT: Sekhon, Jaspreet
APPLICANT: Sekhon, Jaspreet
TITLE OF INVENTION: CDNA FOR HUMAN METHYLENETETRAHYDROFOLATE
TITLE OF INVENTION: REDUCTASE AND USES THEREOF
FILE REFERENCE: 04844/006001
CURRENT FILING DATE: 2000-12-01
CURRENT FILING DATE: 2000-12-01
RATIOR APPLICATION NUMBER: US 09/258,928
PRIOR APPLICATION NUMBER: US 09/258,928
PRIOR FILING DATE: 1999-03-01
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
USEQ ID NO 3
SEQ ID NO 3
LENGTH: 2219
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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; LOCATION: (13)...(1983)
US-09-728-910-3
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Best Local Similarity 53.3%;
Matches 293; Conservative
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                                                                                                                                        181 TAGACCTATCAAGGACAATGAAGAAGCTGTCAAGGCTTATGGAATTCACCTGGGAACTG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             358 TITCTAGGICCTTACCTTGGAGACGCCCTGCAAATGTTTTCCGTGTTAAAGAAGATGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      983 ACCGCGAGATGGCTACCACAGAGGTGCTGAAGCGCCTGGGGATGTGGACTGAGGACCCCA 1042
                                                                                                                                                                                                                                803 CCCTTCGGCAGCTTGTGAAGCTGTCCAAGCTGGAGGTGCCACAGGAGATCAAGGACGTGA 862
                                                                                                                                                                                                                                                                                                                   743 CCGACATGGGCATCACTTGCCCATCGTCCCCGGGATCTTTCCCATCCAGGGCTACCACT 802
                                                                                                                                                                                                                                                                                                                                                                                                             683 TCATCATCACGCAGCTTTTCTTTGAGGCTGACACATTCTTCCGCTTTGTGAAGGCATGCA 742
                                                                             241 AAATGTGCAAAAAAGATTTTAGCTCATGGAATTAAGACAT ---TGCATCTTTATACACTAA 297
                                                                                                                                                                                                                                                                         121 GCTTTATCCGCATGACTGGGTTTTGCAAAACAAAGATACCAGCTGACATTATGGCTGCTT 180
  298 ATATGGAGAAATCTGCATTGGCAATACTAATGAACCTTGGCCTAATTGAAGAGTCCAAAG 357
                                                                                                                                                                                                                                                                                                                                                              61 GCCAAATTGGAATAACGTGTCCTATTGTACCTGGAATTATGCCCCATTAATAATTACAAGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TGATTGTCACCCAATTATTTTATGATACGGATATATTCCTCAAATTTGTGAACGACTGTC 60
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                                                      GCCTGTGCCAGGAGCTTCTGGCCAGTGGCTTGGTGCCAGGCCTCCACTTCTACACCCTCA
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Sequence 1, Application US/09931795

Publication No. US20020198211A1

GENERAL INFORMATION:
APPLICANT: ROZEN, Rima

TITLE OF INVERTION: CDNA FOR HUMAN METHYLENETETRAHYDROFOLATE

TITLE OF INVERTION: REDUCTASE AND USES THEREOF

FILE REFERENCE: 04844/005003

CURRENT APPLICATION NUMBER: US/09/931,795

CURRENT APPLICATION NUMBER: US/09/931,795

CURRENT FILING DATE: 2001-08-16

PRIOR APPLICATION NUMBER: US 09/592,595

PRIOR FILLNG DATE: 1999-03-01

PRIOR APPLICATION NUMBER: US 09/758,928

PRIOR APPLICATION NUMBER: US 08/738,000

PRIOR APPLICATION NUMBER: US 08/738,000

PRIOR FILING DATE: 1995-05-12

PRIOR APPLICATION NUMBER: US 08/738,000

PRIOR FILING DATE: 1995-05-25

PRIOR FILING DATE: 1995-05-25

PRIOR FILING DATE: 1994-05-26

PRIOR FILING DATE: 1994-05-26

NUMBER OF SEQ ID NOS: 18

SOFTWARE: FastSEQ for Windows Version 4.0

INDEED NO 1

LENGTH: 2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1980)
US-09-931-795-1
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US-09-931-795-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 20.9%;
Best Local Similarity 53.3%;
Matches 293; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 2220
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1220 ACTACCTCTT 1229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1100 GTCCCATCTTCTGGGCCTCCAGACCAAAGAGTTACATCTACCGTACCCAGGAGTGGGACG
                          923 GCCTGTGCCAGGAGCTTCTGGCCAGTGGCTTGGTGCCAGGCCTCCACTTCTACACCCTCA
                                                                                                                                863 TTGAGCCAATCAAAGACAACGATGCTGCCATCCGCAACTATGGCATCGAGCTGGCCGTGA 922
                                                                                                                                                                               181 TAGAGCCTATCAAGGACAATGAAGAAGCTGTCAAGGCTTATGGAATTCACCTGGGAACTG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                      583 TCATCATCACGCAGCTTTTCTTTGAGGCTGACACATTCTTCCGCTTTGTGAAGGCATGCA 742
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                                                                          241 AAATGTGCAAAAAGATTTTAGCTCATGGAATTAAGACAT---TGCATCTTTATACACTAA 297
                                                                                                                                                                                                                               803 CCCTTCGGCAGCTTGTGAAGCTGTCCAAGCTGGAGGTGCCACAGGAGATCAAGGACGTGA 862
                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TGATTGTCACCCAATTATTTATGATACGGATATATTCCTCAAATTTGTGAACGACTGTC
                                                                                                                                                                                                                                                                                                                                    CCGACATGGGCATCACTTGCCCCATCGTCCCCGGGATCTTTCCCATCCAGGGCTACCACT 802
                                                                                                                                                                                                                                                                                                                                                                     GCCAAATTGGAATAACGTGTCCTATTGTACCTGGAATTATGCCCCATTAATAATTACAAGG 120
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                                                                                                                                                                                                                                                                                  GCTTTATCCGCATGACTGGGTTTTGCAAAACAAAGATACCAGCTGACATTATGGCTGCTT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 116.4; DB 9;
Pred. No. 5.9e-24;
0; Mismatches 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60
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CCURRENT FILING DATE: 2000-11-01

PRIOR APPLICATION NUMBER: US 09/258,928

PRIOR FILING DATE: 1999-03-01

NUMBER OF SED ID NOS: 15

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO.1

LENGTH: 2220

TYPE: DNA

ORGANISM: Homo Sapiens
FEATURE:
RAME/KEY: CDS
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US-09-728-910-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 20.9%;
Best Local Similarity 53.3%;
Matches 293; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09728910 Patent No. US20010025030A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1100
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983 ACCGCGAGATGGCTACCACAGAGGTGCTGAAGCGCCTGGGGATGTGGACTGAGGACCCCA 1042
                                                                                                                                                                                                    863 TTGAGCCAATCAAAGACAACGATGCTGCCATCCGCAACTATGGCATCGAGCTGGCCGTGA
                                                                                                                                                                                                                                                                                                                                                                                                         743 CCGACATGGGCATCACTTGCCCCATCGTCCCCGGGATCTTTCCCATCCAGGGCTACCACT
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                                               298 ATATGGAGAAATCTGCCATTGGCAATACTAATGAACCTTGGCCTAATTGAAGAGTCCAAAG
                                                                                                  923 GCCTGTGCCAGGAGCTTCTGGCCAGTGGCTTGGTGCCAGGCCTCCACTTCTACACCCTCA
                                                                                                                                           241 AAATGTGCAAAAAGATTTTAGCTCATGGAATTAAGACAT---TGCATCTTTATACACTAA
                                                                                                                                                                                                                                                 181 TAGAGCCTATCAAGGACAATGAAGAAGCTGTCAAGGCTTATGGAATTCACCTGGGAACTG
                                                                                                                                                                                                                                                                                                         803 CCCTTCGGCAGCTTGTGAAGCTGTCCAAGCTGCGAGGTGCCACAGGAGATCAAGGACCTGA
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983 ACCGCGAGATGGCTACCACAGAGGTGCTGAAGCGCCTGGGGATGTGGACTGAGGACCCCA 1042 AATACCCACATGGGGGTGATTCCTGTAATCCATCATATGGTGCATTATCTGATT 537 AGTTCCCTAACGGCCGCTGGGGCAATTCCTCTTCCCCTGCCTTTGGGGAAGCTGAAGGACT 1219 GTCCCATCTTCTGGGCCTCCAGACCAAAGAGTTACATCTACCGTACCCAGGAGTGGGACG 1159 GTCCAATCTTTTGGGCAAATCGACCAAAAAGCTACATATCAAGGACCATAGGATGGGATC 477 GGCGTC---CCCTACCCTGGGCTCTCAGTGCCCACCCCAAGCGCCGAGAGGAAGATGTAC 1099 ATATGGAGAAATCTGCATTGGCAATACTAATGAACCTTGGCCTAATTGAAGAGTCCAAAG TTTCTAGGTCCTTACCTTGGAGACGCCCTGCAAATGTTTTCCGTGTTAAAGAAGATGTCC 417

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APPLICANT: Rozen, Rima
APPLICANT: Sekhon, Jaspreet
TITLE OF INVENTION: CDNA FOR HUMAN METHYLENETETRAHYDROFOLATE
TITLE OF INVENTION: REDUCTASE AND USES THEREOF
FILE REFERENCE: 04844/006001 Score 116.4; DB 10; Length 2220; Pred. No. 5.9e-24; 0; Mismatches 251; Indels 6;

6; Gaps

2

922 297

240

358 TTTCTAGGTCCTTACCTTGGAGACGCCCTGCAAATGTTTTCCGTGTTAAAGAAGATGTCC

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RESULT 9
US-09-294-093B-4653
Sequence 4653, Application US/09294093B
PAtent No. US20010051335A1
GENERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath, V.
APPLICANT: Sherman, Bradley, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20020013958A1 700457642H1
: NAME/KEY: unsure
: LOCATION: 2, 165, 173, 180
: OTHER INFORMATION: a, t, c, g, or other
US-09-923-876-5753
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APPLICANT: Ladyadi, Raghunath V.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
FILE REFERENCE: PL-0012-1 CON
CURRENT APPLICATION NUMBER: 05/09/923,876
CURRENT EPLING DATE: 2001-08-06
FRIOR FILLING DATE: 2001-08-06
PRIOR FILLING DATE: 1999-04-21
PRIOR FILLING DATE: 1999-05-23
PRIOR FILLING DATE: 1999-05-23
PRIOR FILLING DATE: 1999-05-25
RUMBER OF SEQ ID NOS: 6332
SEQ ID NO 5753
SEQ ID NO 5753
LENGTH: 181

TENES. P.N. 1
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Best Local Similarity
Matches 136; Conserva
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ORGANISM: Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   397 TCCGTGTTAAAGAAGATGTCCGTCCAATCTTTTGGGCAAATCGACCAAAAGCTACATAT 456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        457 CAAGGACCATAGGATGGGATCAATACCCACATGGGCGTTGGGGGTGATTCCTGTAATCC 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 TCCGTGTTAAAGAGGATGTTCGACCTATATTCTGGGCCAACAGACCAAAGAGCTATCTTA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GNTTAATTGAGGAGTCCAAGGTTTCAAGGCCATTACCTTGGAGGCCAGCGACTAATGTTT 60
Lalgudi, Raghunath, V. Ito, Laura, Y. Sherman, Bradley, K.
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APPLICANT: Renz Andreas
APPLICANT: Renz Andreas
APPLICANT: Renz Andreas
APPLICANT: Cirpus, Petra
APPLICANT: Cirpus, Petra
APPLICANT: Cirpus, Petra
APPLICANT: Fraund, Andreas
APPLICANT: Fraund, Markus
APPLICANT: Schmidt, Ralf-Michael
APPLICANT: Duwenig, Elke
APPLICANT: Schmidt, Ralf-Michael
APPLICANT: Duwenig, Elke
APPLICANT: Schmidt, Ralf-Michael
APPLICANT: Schmidt, Ralf-Mich
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FEATURE:
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20010051335A1 700354741H1
LOCATION: 14
LOCATION: 14
LOCATION: 14
LOCATION: 14
LOCATION: 07 OTHER INFORMATION: 07 OTHER INFORM
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                                          ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(409)
; OTHER INFORMATION: 62_mm20_c10rev
US-09-734-017A-63
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US-09-734-017A-63
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SEQ ID NO 4653
LENGTH: 159
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.1/WordPerfect SEQ ID NO 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 63, Application Upatent No. US20020142422AJ
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Best Local Similarity 76.6
Matches 118; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR ADPLICATION NUMBER: 60/171,100 PRIOR FILING DATE: 1999-12-16 NUMBER OF SEQ ID NOS: 87
                                                                                                                                                                                                                                                                                    LENGTH: 409
TYPE: DNA
ORGANISM: Physcomitrella
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        508 GTAATCCATCATATGGTGCATTATCTGATTATCA 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             448 GCTACATATCAAGGACCATAGGATGGGATCAATACCCACATGGGGGTTGGGGGTGATTCCT 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 GCTATCTTAAAAGGACATTAGGTTGGGATCAGTATCCCCATGGACGGTGGGGGTGATTCTC 125
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Pred. No. 7.9e-19;
0; Mismatches 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36;
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Indels

0; Gaps

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ORDANISM: Saccharomyces cerevisiae FEATURE:
NAME/KEY: CDS
LOCATION: (826)..(2625)
OTHER INFORMATION: DNA construct US-10-113-852A-1
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US-10-113-852A-1
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APPLICANT: Hanson, Andrew D.
APPLICANT: Raymond, Rhonda R.
APPLICANT: Roje, Sanja
TITLE OF INVENTION: Biosynthesis of S-Adenosyl Methionine in a Recombinant Yeast:
TITLE OF INVENTION NUMBER: US/10/113,852A
CURRENT APPLICATION NUMBER: US/20/13,852A
CURRENT FILING DATE: 2001-03-29
PRIOR FALING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Version 3.0
SEQ ID NO 1
LENGTH: 3082
TYPE: NAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/10113852A Publication No. US20020192784A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 12.0%;
Best Local Similarity 49.5%;
Matches 274; Conservative
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Best Local Similarity 79.2%;
Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   1376 TCATCATCACTCAGATGTTTTACGATGTTGATAATTTACTCAACTGGTGTTCCCAAGTTA 1435
                                                                                                                                                                                                                             1496 CCTTCTTGAGAAGGATCCAATGGGGCCAAATCTCCATCCCTCAACATTTCTCGTCCCGAT 1555
            358 TTTCTAGGTC---
                                                                                                                                                                     241 AAATGTGCAAAAAGATTTTAGCTCATGG---AATTAAGACATTGCATCTTTATACACTAA 297
                                                                                                                                                                                                                                                       181 TAGAGCCTATCAAGGACAATGAAGAAGCTGTCAAGGCTTATGGAATTCACCTGGGAACTG
                                                                                                                                                                                                                                                                                                                                                         121 GCTTTATCCGCATGACTGGGTTTTGCAAAACAAAGATACCAGCTGACATTATGGCTGCTT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 381 GGCTTTCTCCGCATGACCACCTTT 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 GGCTTTATCCGCATGACTGGGTTT 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   321 GTCAAATTGGTATCAAGGTGCCCATTGTACCTGGTATCATGCCCCATTCAAAATTACAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      261 TCATTATCACCCAGCTGTTTTATGATACCGATATCTTTTTGAAATTTGTGAATGATTGTC 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GCCAAATTGGAATAACGTGTCCTATTGTACCTGGAATTATGCCCATTAATAATTACAA-G 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TGATTGTCACCCAATTATTTTATGATACGGATATATTCCTCAAATTTGTGAACGACTGTC
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                                                   ATATGGAGAAATCTGCATTGGCAATACTAATGAACCTTGGCCTAATTGAAGAGTCCAAAG
                                                                                                                                        AAATGTGTCAAAAATTGCTCGACAGTGGTTACGTTTCTCACTTGCACATCTACACCATGA 1679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 67; DB 9; Length 3082; pred. No. 1.3e-09; 0; Mismatches 255; Indels 24;
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Pred. No. 2.4e-15;
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; SEQ ID NO 1
; LENGTH: 640681
; TYPE: DNA
; ORGANISM: Buchnera sp.
US-09-790-988-1
RESULT 13
US-09-754-853A-1/c
US-09-754-853A-1/c
Sequence 1, Application US/09754853A
Publication No. US20030005491A1
GENERAL INFORMATION:
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US-09-790-988-1
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Patent No. US20020127687A1
GEMERAL INFORMATION:
APPLICANT: SHIGENOBU, SHIDEMI
APPLICANT: WATANABE, HIDEMI
APPLICANT: WATANABE, HIDEMI
APPLICANT: BATTORI, MASAHIRA
APPLICANT: SAKAKI, YOSHIYUKI
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
FILE REFERENCE: 08135/0159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
9.6%; Score 53.4; DB 10; Length 640681;
Best Local Similarity 47.5%; Pred. No. 0.00011;
Matches 159; Conservative 0; Mismatches 176; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/790,988 CURRENT FILING DATE: 2001-02-23 PRIOR APPLICATION NUMBER: JP2000-107160 PRIOR FILING DATE: 2000-04-07 NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50707 TTACTCAGTTCTTTTTAATATTTGAAAGTTATTTGCGTTTTCGAGATAATTGTATTAAAA 50766
                                                                                                                                                               51007 ATATTACTTATTCTATTTGTCATATCTTAGGTCTA 51041
                                                                                                                                                                                                                                                     50947 TAAAAAAATTATCTTGTGAAGGAGTAAAAAATTTTCATTTTTACACTTTAAATCAGTCTG 51006
                                                                                                                                                                                                                                                                                                                                       50887 GTTTAGATGATATATTCACACAGAAAATAATTGGTTCTAGTATAGCTATAGATATGG 50946
                                                                                                                                                                                                                                                                                                                                                                                                                            50827 AACGITTTTCAAGTATGACTAÄTGTTAAAATTCCAAAATGGATGCTTGATATGTTTAATG 50886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50767 ATAAAATATATTGATATTATACCAGGTATTTTACCGGTATGTAATTTTCAGAAATTAA 50826
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                                                                                                                                                                                                         307
                                                                                                                                                                                                                                                                                           247 GCAAAAAGATTTTAGCTCATGGAATTAAGACATTGCATCTTATACACTAAATATGGAGA 306
                                                                                                                                                                                                                                                                                                                                                                                187 CTATCAAGGACAATGAAGCAGCTGTCAAGGCTTATGGAATTCACCTGGGAACTGAAATGT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127 TCCGCATGACTGGGTTTTGCAAAACAAAGATACCAGCTGACATTATGGCTGCTTTAGAGC 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 TCACCCAATTATTTTATGATACGGATATATTCCTCAAATTTGTGAACGACTGTCGCCAAA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCATAGGATG------GGATCAATACCCACATGGGCGTTGGGGTGATTCCTGTAATCCAT 516
                                                                                                                                                                                                         AATCTGCATTGGCAATACTAATGAACCTTGGCCTA 341
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APPLICANT: Parsons, Jeremy U.
APPLICANT: Wang, Ming Li
TITLE OF INVENTION: Nucleic Acid Molecules And
TITLE OF INVENTION: Soybean Cyst Nematode Res
FILE REFERENCE: 38-10(15810)B
CURRENT APPLICATION NUMBER: US/09/754,853A
CURRENT FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 60/174,880
PRIOR APPLICATION NUMBER: US 60/174,880
PRIOR FILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 1119
SEQ ID NO 1
LENGTH: 127197
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; ORGANISM: Glycine max
; FEATURE:
; FEATURE:
; OTHER INFORMATION: Clone ID: 515002_region_G2
US-09-754-853A-1
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US-09-815-242-7047
                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PELICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,778
PRIOR TILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILLING DATE: 2000-12-2
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILLING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 7047
LENGTH: 1266
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APPLICANT: Parnell, Laurence |
APPLICANT: Parsons, Jeremy D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58496 CATCTGGAACAGAAAT 58481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58556 AGAAGGCTACAAATGATATTGAGATACTCCATACAGATACCCTTATCAAGGAGGTACAAG 58497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193 AGGACAATGAAGAAGCTGTCAAGGCTTATGGAATTCACCTGGGAACTGAAATGTGCAAAA 252
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Yamamoto, Robert T.
Xu, H. Howard
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Zyskind, Judith W.
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CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR ETILING DATE: 2000-08-24
PRIOR PELLATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 4584
LENGTH: 2000
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US-09-938-842A-4584/c
; Sequence 4584, Application
; Patent No. US2000378A1
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Search completed: February 23, Job time: 240 secs
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Best Local Similarity 60.6%;
Matches 57; Conservative
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Best Local Similarity
Matches 88; Conserv
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APPLICANT: Wang, Xun
APPLICANT: Zhu, Yun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Harper, Jeff
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NAME/KEY: CDS
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                                                                                                     393 GTTTTCCGTGTTAAAGAAGATGTCCGTCCAATCTTTTGGGCAAATCGACCAAAAAGCTA 451
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                                                                              Conservative
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49.2%; Pred. No. 5
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9 AI900449
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10 AW203249
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15	G065P81	HV_CE	GAEdC	G115P70Y	EST54	QGF8G21.	BI129896 G097P07Y	BE194793 HVSMEh008	QGC21G06	G113P82Y	BE346389 sp25a05.y	sp25c05.	BI921517 EST541420	AI727725 BNLGH1883	BQ471487 HV02J07r	AV915401 AV915401	BI125572 I063P12P	WHE0415_	st14b03.	EST35705	AW649374 EST327828	TaE15007	EST27296	NLGH1126	AW234903 sf20e05.y	BQ471589 HV02003r	BM885389 sal99b11.	Zea mays	EST3	sal39d04	TaLr113	QGC23D15	EST40013	EST40013	EST39690	GAEb0	GAEd00	05762 sac37f08

ALIGNMENTS

Fublic Soybean EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800	
Contact: Shoemaker R/Public Soybean EST Project	MENT
Unpublished (1999)	URNAL
Public Soybean EST Project	TLE
,R., Waterston,R. and Wilson,R.	
,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann	
Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk	
Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers	
,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,	
Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna	JTHORS
1 (bases 1 to 588)	RENCE
Glycine.	
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;	
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;	
<pre>Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;</pre>	
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METHYLENETETRAHYDROFOLATE REDUCTASE ; , mRNA sequence.	
Gm-c1067-1734 5' similar to SW:MTHR_ARATH 080585 PROBABLE	
st42e03.yl Gm-c1067 Glycine max cDNA clone	NOTTON
BF071278 588 bp mRNA linear EST 06-DEC-2001	S
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FEATURES

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High quality sequence stop: 414.
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treatment"
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/db_xref="taxon:3847"
/clone="GeNOME SYSTEMS CLONE ID: Gm-c1067-1734"
/clone_1ib="Gm-c1067"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
Possible reversed clone; similarity on wrong strand This clone i
available through; ResGen, Invitrogen Corp. 2130 South Memorial
Parkway Huntsville, AL 35801 For further information call; (800)
-533-4363 or contact via email: ccu@resgen.com
Seg primer: -40RP from Gibco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AI900449 MRNA LINEAR EST 30.NOV-2 SC07301.Y1 Gm-c1012 Glycine mas CHONA clone GENOME SYSTEMS CLONE Gm-c1012-1441 5' Similar to SW:MYHR_ARATH 080585 PROBABLE GM-C1012-TRAHYDROFOLATE REDUCTASE;, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
Contact: Shoemaker
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seedlings"
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/db_xref="taxon:3847"
/clone="GENOME SYSEMS CLONE ID: Gm-c1012-1441"
/clone_lib="Gm-c1012"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                            Contact: Michael A. Grusak

USDA/ARS Children's Nutrition Research Center

Baylor College of Medicine

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                                                                                                                                                                                   Grusak, M.A.,
,J. and Fras
                                                                                                                                                                                                                                                                                                        EST
TIGR sequence name: MTOAR50TK
MORE information is available at:
Seq primer: SKmod (CTA 9AA CTA gtg
Location/Qualifiers
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                                                                mgrusak@bcm.tmc.edu
                                                                                                                                                                                                  Samac, D.A., Town, C.D., Van Aken, S., Utterback, T.,
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             www.medicago.org
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source
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/clone="pgGPO
Length
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Conservative 91.8%; 0; Score 484.4; DB 13; Pred. No. 1.2e-131; Mismatches 46; Indels 0 Gaps 0

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TAGAGCCTATCAAGGACAATGAAGAAGCTGTCAAGGCTTATGGAATTCACCTGGGAACTG GCTTTATCCGCATGACTGGTTTCTGTAAAACAAAGATACCTGCTGAGATAATGGCTGCTT 279 240 219

AAATGTGCAAAAAGATTTTAGCTCATGGAATTAAGACATTGCATCTTTATACACTAAATA 300

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361 CTAGGTCCTTACCTTGGAGACGCCCTGCAAATGTTTTCCGTGTTAAAGAAGATGTCCGTC CTAGATCCTTACCTTGGAGACGCCCGACAAATGTTTTCCGTGTGAAAGAAGATGTTCGGC 459 420

CAATCTTTTGGGCAAATCGACCAAAAAGCTACATATCAAGGACCATAGGATGGGATCAAT

481 ACCCACATGGGCGTTGGGGTGATTCCTGTAATCCATCATATGGTGCATTATCTGATTATC CAATCTTTTGGGCCAAATCGCCCCAAAAAGCTACATATCAAGGACCATAGGATGGGAACAAT ACCCACATGGGCGTTGGAGTGATTCCGGTAACCCGTCATATGGTGCATTAACTGACTATC

540 519 480

AGTTCATGCGGCCACGTG 558 597

GPOD Medicago truncatula 755 bp mRNA linear EST 20-JUL-2001 cDNA clone pGPOD-2P15 5' end,

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                                                                          TAGAGCCTATCAAGGACAATGAAGAAGCTGTCAAGGCATATGGAATACACCTGGGAACTG
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     J. and Fraser,C.M.

BSTs from developing reproductive tissues of Medicago truncatula Unpublished (2001)

Contact: Michael A. Grucab
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USDA/ARS Children's Nutrition Research Center
Baylor College of Medicine
1100 Bates Street, Houston, TX 77030-2600, USA
Tel: 713-798-7044
Fax: 713-798-7078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGR sequence name: MTOAG92TK
MOTE INFORMATION IS AVAILABLE AT:
Seq primer: SKmod (CTA 9AA CTA 9t9
Location/Qualifiers
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Medicago truncatula

Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids I; Fabales; Fabaceae; Papillionoideae; Trifolieae
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/cultivar="A17"
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/clone_lib="GPOD"
/tissue_type="immature pod walls"
/dev_stage="Immature pods, rangin
days after pollination"
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91.6%;
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Pred. No. 3.5e-131;
0; Mismatches 47;
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                                                                                                                                                                                                                                                                                             Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Email: est@watson.wustl.edu
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 21:
South Memorial Parkway Huntsville, AL 35801 For further inforcall: (800)-533-4353 or contact via email: ccu@resgen.com
call: (800)-533-4353 or contact via email: ccu@resgen.com
Insert Length: 1503 Std Error: 0.00
High quality sequence stop: 405.
Location/Qualifiers
1 673 /Qualifiers
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Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bawers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Watterston, R. and Wilson, R., Public Soybean EST Project Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papliionoideae; Phascoleae
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EST.
/note-"Vector: pBluescript II XR; Site_1: EcoRI; Site_2: XhOI; The mRNA was isolated from roots of Glycine max 'Supernod' plants generously donated by Dr. Gary Stacey. The seedlings were innoculated with Bradyrhizoblum japonicus, strain USDA110 priot to harvest. Stratagene's cDNA synthesis Kit (catalog number 200401) was used to
                                                                                                                                /Organism="Glycine max"
/Ob_xref="taxon:3847"
/Ob_ore="cenome sysTems CLONE ID: Gm-c1028-1245"
/clone_lib="Gm-c1028"
/tissue_type="roots of 'Supernod' plants"
/lab_host="DBHOB"
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STEMS CLONE ID:
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75 ACGTGTCCTATTGTACCTGGAATTATGCCCATTAATAATTACAAGGGCTTTATCCGCATG 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTTTAGCTCATGGAATTAATACATTGCATCTTATACACTAAATATGGAGAAATCGGCA
                      AW203207 579 bp mRNA linear EST 02-DEC-2001 sf27d02.yl Gm-c1028 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1028-1180 5' similar to SW MTHR_ARATH 080585 PROBABLE
METHYLENETETRAHYDROFOLATE REDUCTASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cloned Ffu DNA polymerase, ligated to EcoRI adapters and subsequently phosphorylated. The XhoI site within the first-strand synthesis primer was then restricted by digestion with XhoI; all XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500bp cutoff, using GibcoBRL Life Technologies' cDNA Size Fractionation column. The column eluent was then ligated into Stratagene's pBluescript II XR Predigested vector (pBluescript II SK(+) that has been digested with EcoRI and XhoI, and phosporylated by Stratagene). Both the white and blue colonies appear to contain recombinant plasmids with cDNA inserts, based on size (n=25). This library was constructed by Dr. Paul Keim and Dr. Virginia Coryell."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       synthesize the cDNA. First-strand synthesis was performed with 5-methyl dCTP, hence the ligated cDNA was hemimethylated. A modification of Stratagene's first-strand synthesis primer was used. An 'anchor' nucleotide (V-A,C, or G) was added to the 3' end of the primer [GAGAGAGAGAGAGAGACTAGTCTGAGGT1887] to anchor the primer at the 5' end of the poly(A) tract. After second-strand synthesis, the cDNA ends were filled in with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 466.4; DB 10;
Pred. No. 2.1e-126;
0; Mismatches 11;
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Contact: Shoemaker R/Public Soybean EST Propent Public Soybean EST Project Washington University School of Medicine 4444 Forest Park Parky Box 8501, St. Lou Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp.
South Memorial Parkway Huntsville, AL 35801 For further in
call: (800)-533-4363 or contact via email: ccu@resgen.com
Insert Length: 1543 Std Error: 0.00
High quality sequence stop: 413.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Soybean.
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/db_xref="taxon:3847"
/clone="GENOME SYTEMS CLONE ID: Gm-c1028-1180"
/clone_lib="Gm-c1028"
/tissue_type="Toots of 'Supernod' plants"
/lab_host="DH108"
                          83.6%;
Score 466.4; DB 10;
Pred. No. 2.1e-126;
); Mismatches 11;
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Hillier, L., Kucaba, T., Martin, J., Beck, C.,
Steptoe, M., Theising, B., Allen, M., Bowers
T., Gibbons, M., Pape, D., Harvey, N., Schurk
Shin, T., Jackson, Y., Cardenas, M., McCann
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae
                                                                                                                                                                                                                                                                                                                                                                                                                    BG405762
BG405762.1
Fax: 314 200 1012
Email: estGwatson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
                                                                                                                                                                                                         Shoemaker.R., Keim.P., Vodkin,L., Erpelding.J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier.L., Kucaba,T., Martin,J., Beck.C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Materston,R., and Wilson,R.
                                                                                       Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST |
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. i
Tel: 314 286 1810
Fax: 314 286 1810
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468 bp mRNA linear EST 28-NOV-2001 sac37f08 y1 Gm-c1051 Glycine max CDNA clone GROWNE SYSTEMS CLONE ID: Gm-c1051-4503 5' similar to SW.MTHK_RATH 080585 PROBABLE METHYLENETETRAHYDROFOLATE REDUCTASE ;, mRNA sequence.
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                                                                                       BQ404086

GA_E00066A09f Gossypium arboreum 7-10 dpa fiber library Gossypium arboreum cDNA clone GA_E00066A09f, mRNA sequence.

BQ404086.1 GI:21091773

EST.
                Gossypium arboreum.
Gossypium arboreum
Gossypium arboreum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
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FEATURES
                            421 CAATCTTTTGGGCAAATCGACCAAAAAGCTACATATCAAGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 GCCAAATTGGAATAACGTGTCCTATTGTACCTGGAATTATGCCCCATTAATAATTACAAGG 120
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                                                                                                                                                                                                                           TGGAGAAATCTGCATTGGCAATACTAATGAACCTTGGCCTAATTGAAGAGTCCAAAGTTT
                                                                                                                                                                                                                                                                                                                          AAATGTGCAAAAAGATTTTAGCTCATGGAATTAAGACATTGCATCTTTATACACTAAATA
                                                                                                                                                                                                                                                                                                                                                                                        CAATCTTTTGGGGCAATTGGTCAAAAAGCTTCATATTAAGGAC
                                                                                               CTAGGTCCTTACCTTGGAGACGCCCTTGCAATGTTTTCCGTGTTAAAGAAGATGTTCGGC
                                                                                                                                               CTAGGTCCTTACCTTGGAGACGCCCTGCAAATGTTTTCCGTGTTAAAGAAGATGTCCGTC
                                                                                                                                                                                               TGGAGAAATCGGCATTAGCGATACTAATGAACCTTGGCCTAATTGAAGAGACCAAAGTTT
                                                                                                                                                                                                                                                                                              AAATGTGCAAAAAGATTTTAGCTCATGGAATTAATACATTGCATCTTTATACACTAAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCTTTATCCGCATGACTGGGTTTTGCAAAACAAAGATACCAGCTGACATTATGGCTGCTT 180
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442; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-"Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: XhoI; The cDNA library was constructed from floral meristematic mRNA provided by Dr. Halina Knap of Clemson University. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a xhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the ECORI-KhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRI). This library was constructed in the laboratory of Dr. Randy Shoemaker."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q
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/db_xref="taxon:3847"
/db_xref="taxon:3847"
/clone="cENOME SYSTEMS CLONE ID: Gm-c1051-4503"
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/tissue_type="floral meristematic mRNA"
/lab_host="DH108"
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1. .468
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Pred. No. 1.5e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             429.4; DB 12;
No. 1.5e-115;
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REFERENCE

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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAATCTTTTGGGCAAATCGACCAAAAAGCTACATATCAAGGACCATAGGATGGGATCAAT 480
                                                                                                                                                                                                                                                             CTAGGTCCTTACCTTGGAGACGCCCTGCAAATGTTTTCCGTGTTAAAGAAGATGTCCGTC 420
                                                                                                                                                                                                                                                                                                                                                        TGGAGAAATCTGCATTGGCAATACTAATGAACCTTGGCCTAATTGAAGAGTCCAAAGTTT 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCCAAATTGGAATTAATTGTCCTATCGTGCCGGGTATTATGCCCCATTAATAACTACAAGG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , D. Wood, T.C., Leslie, A. and An integrated analysis of the of the cotton fiber (npublished (2000) Contact: Wing RA Clemson University Genomics In Clemson University (100 Jordan Hall, Clemson, SC 100 Jordan Hall, Clem
                                                                                                                                                                                                                                       CTAAGTCCTTACCTTGGAGACGCCCTGCAAATGTTTTTCGTGTTAAAGAAGATGTTCGTC
                                                                                                                                                                                                                                                                                                                                  AAATGTGCCGCAAGATTTTAGCTCATGGGGTTAAGACATTGCACCTTTATACATTAAACA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCAAATTGGAATAACGTGTCCTATTGTACCTGGAATTATGCCCCATTAATAATTACAAGG 120
     AGTTCATGCGGCCACGTG 558
                                                                          ACCCATATGGGCGATGGGGTGATTCTCGAAATCCGTCCTATGGTGCACTAACAGACCATC
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Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry,D., Wood,T.C., Leslie,A. and Wilkins,T.A.
An integrated analysis of the genetics, development, and evolution of the cotton fiber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total High Quality bases = 504
seq primer: TANTACGACTATAGGG
High quality sequence start: 14
High quality sequence stop: 653.
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Fax: 864 656 4293
Email: rwing@clemson.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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/clone="6A_Ed0066A09f"
/clone_lib="Gossypium arboreum
/tissue_type="Fibers isolated i
dpa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Gossypium arboreum"
/strain="AKA"
/cultivar="8400"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="E. coli"
/note="Yector: pBK-CMY; Site_1: EcoRI; Site_2:
131 c 143 g 197 t
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Pred. No. 2.6e-113;
0; Mismatches 85;
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VERSION
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BF269445
LOCUS
DEFINITION
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AUTHORS
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ORGANISM
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ORIGIN
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Best Local Sim:
Matches 446;
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TGGAGAAATCTGCATTGGCAATACTAATGAACCTTGGCCTAATTGAAGAGTCCAAAGTTT
                                                                                                        AAATGTGCAAAAAGATTTTAGCTCATGGAATTAAGACATTGCATCTTTATACACTAAATA
                                                                                                                                                                        TAGAGGCTATCAAGGACAACGAAGAAGCTGTCAAAGCCTATGGAGTTCACCTTGGAACAG
                                                                                                                                                                                                 TAGAGCCTATCAAGGACAATGAAGAAGCTGTCAAGGCTTATGGAATTCACCTGGGAACTG
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589 bp mRNA linear EST 07-MAR-200: GA_Eb0004L07f Gossypium arboreum 7-10 dpa fiber library Gossypium arboreum cDNA clone GA_Eb0004L07f, mRNA sequence.
BF269445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, US Tel: 864 656 7288 Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wing.R.A., Frisch,D., Yu.Y., Main.D., Rambo,T., Simmons,J., Henry ,D., Wood,T.C., Leslie,A. and Wilkins,T.A. An integrated analysis of the genetics, development, and evolution of the cotton fiber Unpublished (2000) Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
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BF269445.1 GI:11200440
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         il: rwing@clemson.edu
primer: TAATACGACTCACTATAGGG
h quality sequence stop: 585.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Gossyplum arboreum"
/strain="AKA"
/cultivar="8400"
/db_xref="rtaxon:29729"
/clone='GA_Eb0004L07f"
/clone_lib="Gossyplum arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10 dpa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="E. coli"
/note="Vector: pBK-CMV; Site_1: EcoRT; Site_2: XhoI"
112 c 125 g 180 t 2 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71.8%;
85.3%;
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Pred. No. 5.7e-107;
0; Mismatches 77;
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     91 CTGGAATTATGCCCATTAATAATTACAAGGGCTTTATCCGCATGACTGGGTTTTGCAAAA 150
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CTAGGTCCTTACCTTGGAGACGCCCTGCAAATGTTTTCGTGTTAAAGAAGATGTTCGTC 465
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barrel medic.

Medicago truncatula

Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Vagnoliophyta; eudicotyledons; core eudicots;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: kvandenb@cbs.umn.edu
Texas A&M University name::726404e
TIGR sequence name:MTGAP64TK
More information is available at.,
http://chrysie.tamu.edu/medicago
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Department of Plant Biology
University of Minnesora
220 BioSci Center, 1445 Gortner Ave, St. Paul, MN 55108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 593)
VandenBosch K., Endre, G., Hur, J., Moore, J., Beremand, P., Ellis, L., Town, C.D., Bowman, C.L., Craven, M.B., Hansen, T.S., Holt, I.B. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE204232 593 bp
EST396908 KVO Medicago truncatula
sequence,
BE204232
BE204232.1 GI:8747517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: VandenBosch K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
                                                                                                                                                             189
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612 625 1738
                                                                                                                                                   /tisue_type="Seedling roots"
//tisue_type="Seedling roots"
//dev_stage="Immediately prior to inoculation with
//dev_stage="Immediately prior to inoculation with
Sinorhizobium meliioti (0 hour)"
//lab_host="E.coli strain XLOLR"
//note="Vector: pBluescript SK -; Site_1: EcoRI; Site_2:
XhoI; CDNA was prepared from polya+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."

137 g 154 t
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                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="pKV0-1418"
/clone_1ib="KV0"
                                                                    71.5%;
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                                                ore 399.2; DB 10; ed. No. 1.3e-106; Mismatches 43;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE433609 558 bp mRNA linear EST 18-MA EST400138 tomato breaker fruit, TIGR Lycopersicon esculentum clone cLEG1602, mRNA sequence.
BE433609
BE433609.1 GI:9431452
EST.
                                                                                                                                                                                                                                                                                                               Email: http://www.genome.clemson.edu/orders/index.html prime sequence.
                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
Contact: CUGI
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, UG
                                                                                                                                                                                                                                                                                                                                                                                                                                            Generation of ESTs from tomato fruit tissue, Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E.,
Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M.,
Niemman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lycopersicon.
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/db_xref="faxon:081"
/db_xref="faxon:081"
/clone="cLEG1602"
/clone_lib="tomato breaker fruit, TIGR"
/tissue_type="Pericarp"
/dev_stage="fyreaker"
/lab_host="SOLR"
/lab_host="SOLR"
/lab_host="SOLR"
/ste="Yector: pBluescriptSKmCUadapt; Site_1: EcoR1;
Site_2: Xhoi; Fruit were harvested at the breaker stage
(first sign of lycopene accumulation on the blossom end
the fruit). Fruit were cut in half and the seeds and
                                                                                                                                                                                                                        /organism="Lycopersicon esculentum"
/cultivar="TA496"
                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                          USA
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                                                                                                                       i (bases 1 to 556)
Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C. Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and J.
                                                                                                                                                                                                                                                                          BE433601
BE433601.1 GI:9431444
EST.
                                     Unpublished (2000)
Contact: CUGI
Clemson University Genomics
Clemson University
100 Jordan Hall, Clemson, SC
                                                                                                                     Nierman, W.,
,S.D.
                                                                                                                                                                                                    Lycopersicon esculentum
Eukaryota; Viridiplantee; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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EST400130 tomato breaker fruit,
Clone CLEG16M10, mRNA sequence.
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                         http://www.genome.clemson.edu/orders/index.html
Location/Qualifiers
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TIGR Lycopersicon
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                     BQ863196

GGC23D15.yg.abl QG_ABCDI lettuce salinas Lactuca sativa
QGC23D15, mRNA sequence.

BQ863196

BQ863196

BQ863196.1 GI:22248661

FST.

Lactuca sativa.

Lactuca sativa.

Lactuca sativa.

Endruca sativa.

Endruca sativa.

Spermatophyta; Wagnoliophyta; Embryophyta; Tractuca sativa.

Asteridae; euasterids II; Asterales; Asteraceae; Lactuca lactuca; Lactuca sativa.
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436; Conservative
             Lactuca.
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/clone_lib="tomato breaker f
/tissue_type="ferricarp"
/dev_stage="breaker"
/lab_host="SOLR"
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/cultivar="TA496"
/db_xref="taxon:4081"
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81.5%;
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Pred. No. 5.
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es 99;
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r EST sativa

14-AUG-2002 CDNA clone

480 440 420 380 360 320 300 260 240 200 180

Lactuceae;

a; Tracheophyta; eudicots;

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JOURNAL COMMENT
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CAATCTTTTGGGCAAATCGACCAAAAAGCTACATATCAAGGACCATAGGATGGGATCAAT
                                    CAAGACCACTTCCATGGAGGAGACCTACTAACCTTTTCCGTCTTAAAGAAGATGTTAGGC
                                                                                                                           TGGAGAAATCTGCATTGGCAATACTAATGAACCTTGGCCTAATTGAAGAGTCCAAAGTTT 360
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                                                                   CTAGGTCCTTACCTTGGAGACGCCCTGCAAATGTTTTCCGTGTTAAAGAAGATGTCCGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Department of Vegetable Crops, R.W.Michelmore University of California at Davis (UCD) Asmundson Hall, UCD, Davis, CA 95616, USA Tel: 1-(530)-742-1742 Fax: 1-(530)-752-9659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Lin, H., van Damme, M., Lavelle, D., Chevaller, P., Ziegle, J., Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K.

Lettuce and Sunflower ESTs from the Compositae Genome Project http://compgenomics.ucdavis.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
belongs to contig QG_CA_Contig1724, see http://cgpdb.uc
for details.
plate: QGC23 row: D column: 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Alexander Kozik [R.W.Michelmore]
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TAG_TISSUB-flowers environmental stress
TAG_SEG-CGAATGCGGG"
188 t
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/clone="06C23D15"
/clone_lib="06C_ABCDI lettuce salinas"
/lab_host="E.coli"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66.2%;
78.9%;
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Pred. No. 9.2e-98;
0; Mismatches 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
JOURNAL
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 135
                                141
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Matches 431;
                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                      21 TATGATACGGATATATTCCTCAAATTTGTGAACGACTGTCGCCAAATTGGAATAACGTGT 80
                                          TTTTGCAAAACAAAGATACCAGCTGACATTATGGCTGCTTTAGAGCCTATCAAGGACAAT 200
                                                                                                                         CCTATTGTACCTGGAATTATGCCCCATTAATTACAAGGGCTTTATCCGCATGACTGGG 140
TTCTGCAAAACTAAGATTCCAGCTGAGATTACTGCTGCCTTGGATCCTATTAAAGACAAT 194
                                                                                               CCTATTGTTCCTGGCATAATGCCAATAAATAACTACAAAGGATTTGTGCGCATGACTGGA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCCACATGGGCGTTGGGGTGATTCCTGTAATCCATCATATGGTGCATTATCTGATTATC 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGTTCATGAGGCCACGTG
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BG904512
BG904512.1 GI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: scioutier@em.agr.ca
was cloned directionally, not a
primer were from the 5' end (sa
Average inset size is >2.2 kb
Plate: 132 row: G column: 08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cereal Research Centre, Agriculture and Agri-food Canada
195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
Tel: (204) 983-2340
Fax: (204) 983-4604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wheat functional generation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2001)
Contact: Dr. Sylvie Cloutier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bread wheat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BG904512 652 bp mRNA linear EST US-TALTI132G08R TaLT1 Triticum aestivum cDNA clone TaLT1132G08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                     194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        primer: M13 Reverse
                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="Leaf tissue"
/dev_stage="14 Days old"
/lab_host="E, coli XLOLR"
/note="Vector: Lambda ZapII; mass excised in plasmid
/note="Teconic Form wheat NII Thatcher Lil 24 hours after
inoculation with leaf rust pathogen Puccinia triticina
race BBB carrying the avirulence gene Avr1."
a 134 c 156 g 168 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Triticum aestivum"
/cultivar="Thatcher Lr1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="TaLr1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:4565"
/clone="TaLr1132G08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                65.7%;
80.1%;
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omics - Thatcher Lrl
                                                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                                                                Score 366.8; DB 12; Pred. No. 4.6e-97;
                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                           107;
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r1132G08 5',
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RESULT 15
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GATTCCTGTAATCCATCATATGGTGCATTATCTGATTATCAGTTCATGCGGCCACGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATACTAATGAACCTTGGCCTAATTGAAGAGTCCAAAGTTTCTAGGTCCTTACCTTGGAGA 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTCATGGAATTAAGACATTGCATCTTATACACTAAATATGGAGAAATCTGCATTGGCA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGGAGGCTGTGAAAGCATATGGAATCCACCTTGGTACTGAGATGTGCAAGAAAATTTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCAAAAAGCTACATATCAAGGACCATAGGATGGGATCAATACCCACATGGGCGTTGGGGGT 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C. Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R., and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycine max

Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae

Glycine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BM526290 569 bp mRNA linear EST 19 sal39d04.y1 Gm-c1059 Glycine max cDNA clone SOYBEAN CLONE Gm-c1059-4400 5' similar to TR:Q9SUJO Q9SUJO METHYLLENETETRAHYDROFOLATE REDUCTASE;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST
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BM526290.1 GI:18731158
                                                                                                                                                                                                                                                                                                                                     This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact: ccu@resgen.com web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Public Soybean EST Project Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 soybean
                                                                                                                                                                                                                                                                                    www.resgen.com
Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Shoemaker R/Public Soybean EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 569)
                                                                                                                                                                                                                                                               quality sequence stop:
                                                   /organism="Glycine max"
/db_xref="taxon:3847"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-c1059-4400"
/clone_lib="cm-c1059"
/clone_lib="cm-c1059"
/tissue_type="Whole seedling, 2 week old, etiolated"
/lab_host="DH10B"
                                                                                                                                                                                                                                 Location/Qualifiers
                             /note="Vector:
pBluescript
library was
                                                                                                                                                                                                                                                                 422.
     constructed from
                             II SK+; Site_1: EcoRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Louis, MO
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isolated
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BASE COUNT
ORIGIN
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Best Local s
Matches 370
                                                                                                                                                                                                                                                                                                                                 121 GCTTTATCCGCATGACTGGGTTTTGCAAAACAAAGATACCAGCTGACATTATGGCTGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190 TGATTGTCACTCAGTTATTTTATGATACGGATATATTCCTCAAATTTGTGAACGACTGTC 249
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CTAGGTCCTTACCTTGGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                    GCCAAATTGGAATAACGTGTCCTATTGTACCTGGAATTATGCCCATTAATAATTACAAGG 120
                                                                                                                                                                 AAATGTGCAAAAAAGATTTTAGCTCATGGAATTAAGACATTGCATCTTTATACACTAAATA
                                                                                                                                                                                                                                                  TAGAGCCTATCAAGGACAATGAAGAAGCTGTCAAGGCTTATGGAATTCACCTGGGAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGATTGTCACCCAATTATTTATGATACGGATATATTCCTCAAATTTGTGAACGACTGTC
                                                                                                                                                                                                                                                                                                                                                                                            GCCAAATTGGAATAACGTGCCCTATTGTACCTGGAATTATGCCCCATTAATAATTACAAGG
                                                                                                                                                                                                                          GCTTTATCCGCATGACTGGGTTTTGCAAAACAAAGATACCAGCTGACATTATGGCTGCTT
                                                           TGGAGAAATCGGCATTAGCGATACTAATGAACCTTGGCCTAATTGAAGAGACCANAGTTT
                                                                                                  TGGAGAAATCTGCATTGGCAATACTAATGAACCTTGGCCTAATTGAAGAGTCCAAAGTTT
                                                                                                                                           AAATGTGCAAAAAGATTTTAGCTCATGGAATTAATACATTGCATCTTTATACACTAAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 97.4
70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from 2 week old etiolated whole seedlings of p1468916.
Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI- XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DHIOB host cells (Gibco BRL). This library was constructed in the laboratory of Dr. Randy Shoemaker at Iowa state university."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 364.6; DB 1
Pred. No. 1.9e-96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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Search completed: February 14, Job time: 2202 secs 2003, 21:53:04

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Title:
Perfect score:
Sequence:
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Maximum Watch 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Published_Applications_AA:*

1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

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8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

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10: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

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14: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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2187
1 ARVIVIQLEYDIDIELKEVN.....VSLVDNDYINGDLEAVEADE 408
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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601	280	443	385	394	608	347	2710	305	349	326	136	191	599	660	660	656	656	592	Length DB
10	5	ø	9	9	9	10	9	9	10	٥	10	10	9	10	9	10	ڡ	9	; ; ;
US-09-864-761-46473	NS-09-823-356-7	US-09-738-626-6203	US-09-992-331-18	US-10-071-338-17	US-10-003-392-2	US-09-911-888-23	US-10-153-273-12	US-09-943-702-5	US-09-919-935-2	US-09-738-626-5879	US-09-734-017A-64	US-09-734-017A-62	US-10-113-852A-2	US-09-728-910-2	US-09-931-795-2	US-09-728-910-4	US-09-931-795-4	US-10-113-852A-4	ID
Sequence 46473, A	Segmence 7 Appli	620	Sequence 18, Appl	Sequence 17, Appl	Sequence 2, Appli	Sequence 23, Appl	Sequence 12, Appl	Sequence 5, Appli	Sequence 2, Appli	Sequence 5879, Ap	Sequence 64, Appl	Sequence 62, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli	Description

	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20
	78	78	78	78	78	78.5	78.5	78.5	78.5	78.5	78.5	78.5	78.5	78.5	78.5	79	79	79	79	80	81	81.5	81.5	82	83	83.5
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	1241	602	541	532	347	615	611	323	323	323	323	323	323	323	284	402	381	381	381	26926	410	650	650	291	5795	653
	9	10	10	10	10	9	10	10	10	10	10	10	10	9	10	10	10	10	10	9	10	10	9	9	10	9
AT TOMPINE	US-10-007-270-17	US-09-815-242-12896	US-09-815-242-5807	US-09-965-553-8	US-09-815-242-11680	US-10-003-392-17	US-09-829-549A-48	US-09-903-325A-7	US-09-903-323A-7	US-09-903-188A-7	US-09-903-171A-7	US-09-903-187A-7	US-09-903-180B-7	US-09-903-170C-7	US-09-815-242-13298	US-09-983-931-6	US-09-292-973-20	US-09-292-973-5	US-09-962-646-16	US-09-759-508B-2	us-09-905-176-26	US-09-993-038-2	US-09-993-241-2	US-10-017-910-6	US-09-815-242-12610	US-10-206-443-2
	Sequence 17, Appl	Sequence 12896, A	Sequence 5807, Ap	Sequence 8, Appli	Sequence 11680, A	Sequence 17, Appl	Sequence 48, Appl	7,	Sequence 7, Appli	Sequence 13298, A	Sequence 6, Appli	Sequence 20, Appl	Sequence 5, Appli	Sequence 16, Appl	Sequence 2, Appli	Sequence 26, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 6, Appli	Sequence 12610, A	Sequence 2, Appli					

## ALIGNMENTS

Ф	Фр	Фр	Qу Дъ	Que Bes Mat	RESULT 1  Sequen  Sequen  PUBLIC  GENERA  APPLI  AP
181 DYOPMRDRARDKKLVEEMAVPLKSVEDIYERFFLYCLGKLRSNPWSELDGLOPETKIINE 240 	121 KYSRSLÞWRRÞANYFRYKEDYRÞIFWANRÞKSYISRŤIGWÐQYÞHGRWGDSCNÞSYGALS 180 	61 AALEPIKDNEEAVKAYGIHLGTEMCKKILAHGIKTLHLYTLNMEKSALAILMNLGLIEES 120 	1 ARVIVTQLEYDTDIFLKEVNDCRQIGITCPIVPGIMPINNYKGFIRMTGFCKTKIPADIM 60   :	Query Match 81.3%; Score 1777; DB 9; Length 592; Best Local Similarity 78.6%; Pred. No. 7.2e-161; Matches 319; Conservative 44; Mismatches 43; Indels 0; Gaps 0;	RESULT 1 US-10-113-852A-4 Sequence 4, Application US/10113852A Sequence 4, Application US/20194841 Sequence 4, Application US/2020.9278481 Seprent Information: Seprent Informati

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580 FMFWKDEAFALWIERWGKLYEEESPSRTIIQYIHDNYFLVNLVDNDFPLDNCLWQVVED 638

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CURRENT APPLICATION NUMBER: US/09/931,795
CURRENT FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: US 99/592,595
PRIOR FILING DATE: 2000-06-12
PRIOR APPLICATION NUMBER: US 99/256,928
PRIOR FILING DATE: 1999-03-01
PRIOR FILING DATE: 1997-02-12
PRIOR FILING DATE: 1997-02-12
PRIOR FILING DATE: 1997-02-12
PRIOR FILING DATE: 1997-02-12
PRIOR FILING DATE: 1997-05-15
PRIOR FILING DATE: 1997-05-25
PRIOR APPLICATION NUMBER: GE 9410620.0
PRIOR FILING DATE: 1997-05-25
PRIOR APPLICATION NUMBER: GB 9410620.0
PRIOR FILING DATE: 1997-05-26
PRIOR APPLICATION NUMBER: GB 9410620.0
PRIOR FILING DATE: 1997-05-26
PRIOR
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-931-795-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 44.8%;
Best Local Similarity 44.9%;
Matches 188; Conservative 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/09931795 Publication No. US20020198211A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: CDNA FOR HUMAN METHYLENETETRAHYDROFOLATE TITLE OF INVENTION: REDUCTASE AND USES THEREOF FILE REFERENCE: 04844/005003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    350 FNVWKDEAFEIWSRGWASLYPEDEASRKLYEEVGGSHFLVSLYDNDY-INGDLFAVFAD 407
                                                                                                                                                                                                                                                                                                  460 LAAETSILKEELLRVNRQGILTINSQPNINGKPSSDPIVGWGPSGGYVFQKAYLEFTTSR 519
                                                                                                                                                                                                                                                                                                                                                                                231 LOPETKIINEQLEKINTKGFLTINSQPAVNGEKSDSPTVGWGGPGGYVYQKAYVEFFCSK 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             401 KDYYLFYLKSKSPKEELLKMWGEELTSEASVFEVFVLYLSGEPNRNGHKVTCLPWND-EP 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 SDYQ--FMRPRARDKKLYEEWAVPLKSVEDIYERFRLYCLGKLRSN------PWSELDG 230
                                                                                                                                 520 ETAEALLQVLKKYELRVNYHLVNVKGENITNAPELQPNAVTWGIFPGREIIQPTVVDPVS 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          282 DVIEPIKDNDAAIRNYGIELAVSLCQELLASGLVPGLHFYTLNREMATTEVLKRLGMWTE 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     222 ADFILTQLFFEADTFFREVKACTDMGITCPIVPGIFPIQGYHSLRQLVKLSKLEVPQEIK 281
                                                                                                                                                                                                               291 EKLDALVDKCKD-RTSLTYMAVNKDGSWKSNVGQTDVNAVTWGVFPAKEIIQPTIVDPVS 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 AALEPIKDNEEAVKAYGIHLGTEMCKKILAHG-IKTLHLYTLNMEKSALAILMNLGLIEE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ARVIVIQUEYDIGIEKEVNDCRQIGITCPIVPGIMPINNYKGEIRMIGECKIKIPADIM 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WSRSWANLYPEDDPSRKLLEEVKNSYYLVSLVDNNYINGDIFSVFA 592
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RESULT 4
US-09-911-795-2
US-09-921-795-2
Sequence 2, Application US/09931795
Publication No. US20020198211A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ROZEN, Rima
FITLE OF INFUNITION: CONA FOR HUMAN METHYLENETETRAHYDROFOLATE
FILE PETHYLENITION: REDUCTASE AND USES THEREOF
FILE REFERENCE: 04644/005003
CURRENT APPLICATION NUMBER: US/09/931/795
CURRENT FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: US 09/592,595
PRIOR FILING DATE: 2000-06-12
PRIOR FILING DATE: US/00-06-12
PRIOR APPLICATION NUMBER: US 09/258,928
PRIOR APPLICATION NUMBER: US 09/258,928
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; ORGANISM: Homo sapiens
US-09-728-910-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
US-09-728-910-4
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SEQ ID NO 4
LENGTH: 656
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APPLICANT: Sekhon, Jaspreet
APPLICANT: Sekhon, Jaspreet
TITLE OF INVERTION: CDNA FOR HUMAN METHYLENETETRAHYDROFOLATE
TITLE OF INVENTION: AREDUCTASE AND USES THEREOF
FILE REFERENCE: 04844/006001
CURRENT APPLICATION NUMBER: US/09/728,910
CURRENT FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: US 09/258,928
PRIOR FILLING DATE: 1999-03-01
NUMBER OF SEQ ID NOS: 15
NUMBER OF SEQ ID NOS: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           460 LAAETSLLKEELLRVNRQGILTINSQPNINGKPSSDPIVGWGPSGGYVFQKAYLEFFTSR 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  231 LQPETKIINEQLEKINTKGFLTINSQPAVNGEKSDSPTVGWGGPGGYVVQKAYVEFFCSK 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        401 KDYYLFYLKSKSPKEELLKMWGEELTSEASVFEVFYLYLSGEPURNGHKYTCLPWND-EP 459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           282 DVIEPIKDNDAAIRNYGIELAVSLCQELLASGLVPGLHFYTLNREMATTEVLKRLGMWTE 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         222 ADFIITQLFFEADTFFRFVKACTDMGITCPIVPGIFPIQGYHSLRQLVKLSKLEVPQEIK 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FNVWKDEAFEIWSRGWASLYPEDEASRKLVEEVGGSHFLVSLVDNDY-INGDLFAVFAD 407
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PRIOR APPLICATION NUMBER: US 08/738,000
PRIOR FILING DATE: 1997-02-12
PRIOR FILING DATE: 1995-05-25
PRIOR FILING DATE: 1995-05-25
PRIOR APPLICATION NUMBER: GB 9410620.0
PRIOR FILING DATE: 1994-05-26
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Дb
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US-09-728-910-2
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                                                                            US-09-728-910-2
                                                                                                                                                                                                                                                           Sequence 2, Application US/09728910
Patent No. US20010025030A1
GENERAL INFORMATION:
APPLICANT: Rozen, Rima
APPLICANT: Sekhon, Jaspreet
TITLE OF INVENTION: CDMA FOR HUMAN METHYLENETETRAHYDROFOLATE
TITLE OF INVENTION: REDUCTASE AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 188; Conserv
                                                                                                                                    SOFTWARE:
SEQ ID NO 2
              Matches 188;
                             Query Match 44.8%;
Best Local Similarity 44.9%;
                                                                                                                                                                               FILE REFERENCE: 04844/006001
CURRENT APPLICATION NUMBER: US/09/728,910
CURRENT FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: US 09/258,928
PRIOR FILING DATE: 1999-03-01
                                                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                      LENGTH: 660
TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                     FastSEQ for Windows Version 4.0
              Conservative
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44.9%; Pred. No. 7.2e-85;
tive 79; Mismatches 138;
           79;
           Score 979; DB 10;
Pred. No. 7.2e-85;
79; Mismatches 138;
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RESULT 6
US-10-113-852A-2
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LENGTH: 599
TYPE: PRT
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Best Local Similarity 40...
168; Conservative
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publication No. US20020192784A1
GENERAL INFORMATION:
APPLICANT: Appling, Dean R.
APPLICANT: Raymond, Rhonda R.
APPLICANT: Roje, Sanja
TITLE OF INVENTION: Biosynthesis of S-Adenosyl Methionine in a Recombinant Yeast:
PILE REFERENCE: 119927-1033
CURRENT APPLICATION NUMBER: US/10/113,852A
CURRENT FILING DATE: 2002-03-29
PRIOR APPLICATION NUMBER: 60/280,333
PRIOR APPLICATION NUMBER: 2001-03-30
PRIOR FILING DATE: 2001-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 13 SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                            185 IITQMFYDVDNLLNWCSQVRAAGMDVPIIPGIMPITTYAAFLRRIQWGQISIPQHFSSRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                               4 IVTQLFYDTDIFLKFVNDCRQIGITCPIVPGIMPINNYKGFIRMTGFCKTKIPADIMAAL 63
                                                                                                                                                                                            FNVWKDEAFEIWSRGWASLYPEDEASRKLYEEVGGSHFLVSLYDNDY-INGDLFAVFAD
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                                                     FGDLDLCGSD--LIRQSA--NKCLELWSTP-TSINDVAFLVINYLNGNLKCLPWSDIP-I
                                                                                                                                                                 FNAHPLAVLPWRKSLNPKRKNEEVRPIFWKRRPYSYVARTSQWAVDEFPNGRFGDSSSPA
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QPETKIINEQLEKINTKGFLTINSQPAVNGEKSDSPTVGWGGPGGYVYQKAYVEFFCSKE
                                                                                                        YGAL----SDYQFMRPRARDKKLVEEWAVPLKSVEDIYERFRLYCLGKLRSNPWSELDGL
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40.9%; Pred. No. 8.3e-66;
ative 76; Mismatches 147;
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APPLICANT: Duwenig, Elke
APPLICANT: Schmidt, Ralf-Michael
APPLICANT: Schmidt, Ralf-Michael
TITLE OF INVENTION: Moss genes from Physcomitrella patens encoding proteins involved
TITLE OF INVENTION: Moss genes from Physcomitrella patens encoding proteins involved
TITLE OF INVENTION: Moss genes from Physcomitrella patens encoding proteins involved
TITLE OF INVENTION: Mynthesis of amino acids, vitamins, cofactors, nucleotides and
TITLE OF INVENTION: Involcosides
TILE REFERENCE: BASE-NAE-1331-99-US
CURRENT FILING DATE: 1000-12-12
CURRENT FILING DATE: 1000-12-12
PRIOR APPLICATION NUMBER: 05/171/100
PRIOR PILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin Ver. 2.1/WordPerfect
SEQ ID NO 62
LENGTH: 191
TYPE: PRT
ORGANISM: Physcomitrella patens
US-09-734-017A-62
                                                                                                                                                                                                                                                         US-09-734-017A-64
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US-09-734-017A-62
APPLICANT: Lerchl, Jens
APPLICANY: Renz, Andreas
APPLICANT: Ehrhardt, Thomas
APPLICANT: Reindl, Andreas
APPLICANY: Cirpus, Petra
APPLICANY: Bischoff, Friedrich
APPLICANT: Frank, Markus
                                                                                                                                                                           Sequence 64, Application US/09734017A Patent No. US20020142422A1 GEMERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 33.9%; Score 742; DB 10; Best Local Similarity 79.9%; Pred. No. 4.1e-63; Matches 135; Conservative 14; Mismatches 20;
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APPLICANT: Renz,
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                                                                                                                                                                                                                                                                                                                                                                            123 SRSLPWRRPANVFRVKEDVRPIFWANRPKSYISRTIGWDQYPHGRWGDS 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       419 NDEINPIKAHLIELNQHSIITINSQPQVNGIRSNDKIHGWGPKDGYVYQKQYLEFMLPKT 478
                                                                                                                                                                                                                                                                                                                                                       123 SRPLPWRPPTNSKRTKEDVRPIFWANRPRSYISRTTSWDDFPRGRWGDT 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           539 LAWKEEFYHILNEWKLNMNKYDKPHSAQFIQSLIDDYCLVNIVDNDYISPD 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   351 NVWKDEAFEIWSRGWASLYPEDEA-SRKLVEEVGGSHFLVSLVDNDYINGD 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 VIITQLFYDTDIFLKFVNDCRQIGIKVPIVPGIMPIQNYKGFLRMTTLCKTKVPAEIMAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 VIVTQLFYDTDIFLKFVNDCRQIGITCPIVPGIMPINNYKGFIRMTGFCKTKIPADIMAA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KLDALVDKCKDRTSLTYMAVNKDGSWKSN-VGQTDVNAVTWGVFPAKEIIQPTIVDPVSF 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEPIKONDEAVRAYGIHLGTEMCKKILAHDIRTLHLYSLNLEKSYLGILQNLGLIDFSRV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         {\tt KLPKLIDTLKNNEFLTYFAIDSQGDLLSNHPDNSKSNAVTWGIFPGREILQPTIVEKISF}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reindl, Andreas
Cirpus, Petra
Bischoff, Friedrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Renz, Andreas
Ehrhardt, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Freund, Annette
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US-09-738-626-5879
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Best Local
                                                                                                                                                                                                         Matches
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TYPE: PRT
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                                                                                                                                                                                                      l Similarity
36; Conser
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37; Conser
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APPLICANT: HAYASHI, MIKIRO
APPLICANT: COCHIA, KEIKO
APPLICANT: COCHIA, KEIKO
APPLICANT: COCHIA, KEIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKHIHO
APPLICANT: KERDA, MASATO
APPLICANT: CZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR APPLICATION NUMBER: JP 09/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR TILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ ID NO 5879
LENGTH: 326
                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT ; ORGANISM: Corynebacterium glutamicum US-09-738-626-5879
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APPLICANT: Duwenig, Elke
APPLICANT: Duwenig, Elke
APPLICANT: Schmidt, Ralf-Michael
TITLE OF INVENTION: Moss genes from Physcomitrella patens encoding proteins involv
TITLE OF INVENTION: Synthesis of amino acids, vitamins, cofactors, nucleotides an
TITLE OF INVENTION: Incleosides
FILE REFERENCE: BASF-NAE-1331-99-US
CURRENT APPLICATION NUMBER: US/09/734,017A
CURRENT APPLICATION NUMBER: 60/171,100
PRIOR FILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin Ver. 2.1/WordPerfect
SEQ ID NO 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5879, Application US/09738626 Publication No. US20020197605A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
                                                                                                               189 AEYSITQMFFDVEDYLRLRDRLVAADPIHGAK-----PIIPGIMPITSLRSVRRQVELS 242
243 GAQLPSQLEESLVRAANGNEEANKDEIRKVGIEYSTNMAERLIAEGAEDLHFMTLNFTRA 302
                                                    52 KTKIPADIMAAL-EPIKDNEEA----VKAYGIHLGTEMCKKILAHGIKTLHLYTLNMEKS 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87 VIITQLEYDTDIELKEVNDCRQIGIKVPIVPGIMPIQNYKG 127
                                                                                                                                                                   1 ARVIVTQLFYDTDIFLKF------VNDCRQIGITCPIVPGIMPINNYKGFIRMTGFC 51
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                                                                                                                                                                                                                           7.2%; Score 158; DB 9; Length 326; 27.7%; Pred. No. 3.3e-07; tive 28; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 199; DB 10;
Pred. No. 1.2e-11;
1; Mismatches 3;
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303 TQEVLYNLGM 312

107

ALAILMNLGL 116

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; LENGTH: 349
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-919-935-2
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CUURRENT APPLICATION NUMBER: US/09/919,935
CUURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: DE 10053942.4
PRIOR FILING DATE: 2000-08-02
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: DE 10109686.0
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US 60/294,279
PRIOR FILING DATE: 2001-05-31
PRIOR FILING DATE: 2001-05-31
                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-943-702-5
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Patent No. US20020049305A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.1 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/09943702 Publication No. US20030022322A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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APPLICANT: GREISSINGER, DIETER
TOTALICANT: GEORG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: GREISSINGEK, DIELL.
APPLICANT: THIERBACH, GEORG
TITLE OF INVENTION: NUCLEGATIOE SEQUENCES WHICH CODE FOR THE METF GENE
FTI.R REFERENCE: 211712USOX
TIC/19/919,935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: BATHE, BRIGITTE APPLICANT: MOCKEL, BETTINA APPLICANT: PFEFFERLE, WALTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 4
COUNTW...
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BOTH PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      266 GAQLPSQLEESLVRAANGNEEANKDEIRKVGIEYSTNMAERLIAEGAEDLHFMTLNFTRA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        212 AEYSITQMFFDVEDYLRLRDRLVAADPIHGAK-----PIIPGIMPITELRSVRRQVELS
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                                                                                                                                                                                                                                                                                      ROSTECK Jr., Paul R
TITLE OF INVENTION: SAM Operon
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                               APPLICANT: DeHoff, Bradley S.
Rosteck Jr., Paul R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36;
                                                                                                                                                              CITY: Indianapolis
STATE: Indiana
COUNTRY: U.S.
                                                                                                                                                                                                                            ADDRESSEE: Eli Lilly and Company STREET: Lilly Corporate Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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27.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 157; DB 10;
Pred. No. 4.6e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47;
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TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-943-702-5
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US-10-153-273-12
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Patent No. US20020169305A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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             COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/153,273
FILING DATE: 21-May-2002
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/210,288
FILING DATE: <UNknown>
ATTORNEY/ACENT INFORMATION:
NAME: Fuller, Michael
REGISTRATION NUMBER: 35,516
REGISTRATION NUMBER: NIHHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179 ITOMFFRVEDYLRLRDRVAAAGCCTPVIPGIMPATDVRQIARFAELSHATFPEGLARRLE 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239 AARGNPAEGHRIGVEYATAMAGRLLAEGAPGLHYITLNRSTATLEIHRNI 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/943,702
FILING DATE: 31-Aug-2001
CLASSIFICATION: -CUNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: P-10162 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                               ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIKDNEEAVKAYGIHLGTEMCKKILAHGIKTLHLYTLNMEKSALAILMNL 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Webster, Thomas D. REGISTRATION NUMBER: 39,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/955,957 FILING DATE: 1997-10-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                  CITY: Newport Beach
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wellems, Thomas E.
OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
REFERENCE/DOCKET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Su, Xin-zhaun
Wellems mt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sim, Kim L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chitnis, Cheta
Miller, Louis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chetan
    NUMBER: NIH121.1FWDV1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 138; DB 9;
Pred. No. 2.4e-05;
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Sequence 23, Application US/09911888

Patent No. US20020119509A1

GENERAL INFORMATION:
APPLICANT: Koltin, Yigal
APPLICANT: Koltin, Yigal
APPLICANT: Gavilas, Victoria
TITLE OF INVENTION: ESSENTIAL FUNCAL GENES AND THEIR USE
FILE REFERENCE: 06286-062002

CURRENT APPLICATION NUMBER: US/09/911,888

CURRENT FILING DATE: 2001-07-23

PRIOR APPLICATION NUMBER: US 08/965,762

PRIOR FILING DATE: 1997-11-07

NUMBER OF SEQ ID NOS: 35

SOFTMARE: FastSEQ for Windows Version 3.0

SEQ ID NO 23

LENGTH: 347

TYPE: PAT

ORGANISM: Saccharomyces cerevisiae
US-09-911-888-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Plasmodium falciparum SEQUENCE DESCRIPTION: SEQ ID NO: 12: US-10-153-273-12
                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
US-09-911-888-23
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Matches
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TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        546 LKSGKGHDDIEEKLNKFCDEKNGD 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        432 FYDELNKSEYRTVDKFLEKLSNEEICTKVKDEEGGTIDFKNVNSD----STSGASGTNVE 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  226 SELDGLQPETKIINEQLEKINTKGFLTINSQPAVNGEKSD---SPTVGWGGPGGYVYQKA 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          274 TYFHATCNRGERTKGYCRCNDDQVPTY---FDYVPQYLR-----WFEEWAEDFCRKKN 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          330 TWGVFPAKEIIQP-----TIVDPVSFNVWKDEAFEIWSRGWASLY---PEDEASRKLV 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              283 Y-----VEFFCSKEKLDALYDKCKDRT--SLTYMAVNKDGSWKSNVGQTDVNAV 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         384 NQKEQFDKQKKKYDEEIKKYE-----NGASGGSRQKRDAGGTTTTNYDG-----YEKK 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        324 KKIKDVKRNCRGKDKEDKDRYCSRNGYDCEKTKRAIGKLRYGKQCISCLYACNPYVDWIN 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               203 KSVEDIYERFR------LYC------LGKLR------SNPW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           227 -- FGKIYEKLNGAEARYGNDPEFFKLRED----WWTANR-----ETV-WKAITCNAWGN 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 2710 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S----- 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SQGTFYRSKYCQPCPYCGVKKVNNGGSSNEWEEKNNGKCKSG--KLYEPKPDKEGTTITI 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EEVGGSHFLVSLVDN---DYINGD 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 4.5%; Score 97.5; DB 9; 1 Similarity 19.8%; Pred. No. 4.3; 88; Conservative 59; Mismatches 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2710;
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GENERAL INFORMATION: Helphon M.  APPLICANT: Alien, Stephen M.  APPLICANT: Caimi, Perry G.  APPLICANT: Stoop, Johan M.  PITLE OF INVENTION: Fructan Biosynthetic Enzymes  FILE REFERENCE: BB143 US NA  CURRENT FILING DATE: 2001-10-30  PRIOR APPLICATION NUMBER: 60/244,273  PRIOR APPLICATION NUMBER: 60/244,273  PRIOR APPLICATION NUMBER: 60/269,543  PRIOR FILING DATE: 2000-10-10  PRIOR FILING DATE: 2000-10-10  PRIOR APPLICATION NUMBER: 60/269,543  PRIOR FILING DATE: 2000-10-10  PRIOR APPLICATION  PRIOR APP	Best Local Similarity 21.3%; Pred. No. 0.87;  Matches 78; Conservative 57; Mismatches 118; Indels 114; Gaps  Qy 2 RVIVTQLFYDTDIFLKFVNDCRQIGITCPIVPGIMPINNYKGFIRMTGFCKTKIPADIMA 61
25;	22;

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RESULT 15
US-10-071-338-17
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                                                                                                                                                US-10-071-338-17
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Publication No. US20030022321A1
GENERAL INFORMATION:
                                                                                   Query Match
Best Local :
                                                                  Matches
                                                                                                                                                                                                                                                                 TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 394 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            384 -NVARTVVLDRKTGTHLLHWPVEEIESLRSNGQEF 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         371 EDEASRKLVEEVGGSHFL---VSLVDNDYINGDLF 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    328 DNPKLDVGIGLRCDYGKFFASKSLFDPLKKRRVT---WGYVGESDKPDQDLSRGWATIY- 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  332 ------GV------FPAKEIIQPTIVDPVSFNVW------KDEAFEIWSRGWASLYP 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148 YDIEGVLSGSTTVLPNGQIFALYTGNANDFSQLQCKAVPVNISDPLLIEWVKYDGNPILY
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/10/071,338
FILING DATE: 08-Feb-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Valentine, Jill B
REGISTRATION NUMBER: <Unknown>
REFERENCE/DOCKET NUMBER: P31731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              268 NTDMWECVDFYPVSLTNDSALDMAAYGSGIKHVIKESWEGHGMDWYSIGTYDASTDKWTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    298 D----KCKD--RTSLTY-----MAVNKDG------SWKS-----NVGQTDVNAVTW-- 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        208 TPPGIGLKDYRDPSTVWTGPDGKHRMIMGSKRNKTGLVLVYHTTDFTNYVMSDEPLHSVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   255 SQPAVNGEKSDSPTVGWGGPGG-----
                                                               y Match 4.0%; So
Local Similarity 25.2%; Po
hes 38; Conservative 20;
97 HLYTLIMEKSALAILMNIGL-----IEESKVSRSLPWRRPANVFRVKEDVRPIFWANRP 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: UK
ZIP: TWB 9EP
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 0181-9752000
TELEFAX: 0181-9756294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SmithKline Beecham plc et al TITLE OF INVENTION: No. US20030022321Alel compounds NUMBER OF SEQUENCES: 19
                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: Two, New CITY: Brentford STATE: <Unknown>
                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                             STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New Horizons Court,
                                                               Score 88; DB 9
Pred. No. 2;
20; Mismatches
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                                                                                                      DB 9; Length 394
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                                                               55;
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                                                               Indels
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                                                               Gaps
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Search completed: February 12, Job time : 25 secs
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                                                                                                                                                        114 RAFYGIARGFQK----RWADIMGQVYGVGGTLSD-AGERDR-RNRALFEEHWEIIKKAWT 167
                                                                                                                                                                                              151
                                                                            168 TETFTHSGEQWTIPVPDLEFPYEAVRRYGRG 198
                                                                                                                                                                                                                                    57
                                                                                                                                                                                            KSYISRTIGWDQYPHGRWGDSCNPSY---GALSDYQFMRPRARDKKLVEE------
                                                                                                                  ------WAVPLKSVEDIYERFRLYCLG
                                                                                                                                                                                                                                  HFHTEGFEVSNNPIMLGLYLGMQTRHIRVGQMANVLPLHNP---LRLAEDLAMLDHMTRG 113
                    2003, 17:04:30
                                                                                                                    218
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq Maximum DB seq Run Total number of hits satisfying chosen parameters: Scoring table: Sequence: Title: Perfect score: OM protein - nucleic search, using frame\_plus\_p2n model Database : FGAPEXT=7 -YGAPOP=10 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Score length: 0 length: 2000000000 Query Match Length Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext BLOSUM62 US-09-720-451-6 2187 February 12, Published\_Applications\_NA: \* 424239 seqs, 254661826 residues 1 ARVIVTQLFYDTDIFLKFVN......VSLVDNDYINGDLFAVFADF 408 81.3 44.8 44.8 44.8 :/cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
:/cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
:/cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
:/cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
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:/cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*
:/cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
:/cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
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:/cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
:/cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\* GenCore version Copyright (c) 1993 - 2003 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7 1994 2219 2219 2219 2220 2003, 17:03:12; Search time 75 Seconds
(without alignments)
2770.721 Million cell updates/sec DB 9 9 US-10-113-852A-3 US-09-931-795-3 0 US-09-728-910-3 US-09-931-795-1 Ħ SUMMARIES 0.5 0.5 7.0 5.1.3 Compugen Ltd. 848478 Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 1, Appli Description

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RESULT 1 US-10-113-852A-3

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	-10-044-090	9-823-356-2	004-381-3	-10-004-381-4	S-09-927-0	9-070-927	-09-938-842A-	9-738-626-2	9-738-626-2	09-895-382-	0-090-624-	9-738-626-2	-09-964-824A-25	09-967-768A	-09-954-456-	10-071-338-1	-09-925-30	10-071-338-6	-09-070-92	10-003-392	-09-911-888-2	-09-911-88	10-153-273-1	-10-114-170-5	09-943-70	15-09-943-70	-09-943-70	-09-919-935-	9-738-62	-09-790-988-1	-09-734-017A-6	-09-294-093B-4	-09-923-876-150	9-923-876-575	-09-923-876-47	-09-923-876-559	-09-878-574-37	S-09-734-017A-6	-10-113-852A-1	S-09-770-445-	-09-728-910-	
•	equence 37	e 24	equence 37,	40,	ω,	547	9	equence 2702	equence 2703	e 31, App	e 5,	2317,	254,	219	e 92, p	1, A	e 66	6, A	e 78	1, Ar	2	e 22,	11, 7	50,	Ó	4	1,	Sequence 1, Appli	23	equence 1	e 63,	equence 4653,	equence 1503	equence 575	e 476,	e 5596	3765, A	e 61	1, Appli	Sequence 690, Ap	equence 1,	

# ALIGNMENTS

; NAME/KEY: CDS
; LOCATION: (63)..(1841)
; OTHER INFORMATION: DNA construct
US-10-113-852A-3 Sequence 3, Application US/10113852A
Publication No. US20020192784A1
GENERAL INFORMATION:
APPLICANT: Appling, Dean R.
APPLICANT: Hanson, Andrew D.
APPLICANT: Raymond, Rhonda R.
APPLICANT: Roje, Sanja
TITLE OF INVENTION: Biosynthesis of S-Adenosyl Methionine
FILE REFERENCE: 119927-1033 SOFTWARE: PatentIn version 3.0 SEQ ID NO 3 CURRENT APPLICATION NUMBER: US/10/113,852A CURRENT FILING DATE: 2002-03-29 PRIOR APPLICATION NUMBER: 60/280,333 PRIOR FILING DATE: 2001-03-30 NUMBER OF SEQ ID NOS: 13 TYPE: DNA ORGANISM: Arabidopsis thaliana FEATURE: ENGTH: 1994 in a Recombinant Yeast

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Alignment Scores:

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Percent Similarity:
Best Local Similarity:
Query Match:
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PRIOR APPLICATION NUMBER: US 09/592,595
PRIOR FILING DATE: 2000-06-12
PRIOR FILING DATE: 1999-03-01
PRIOR REPLICATION NUMBER: US 09/258,928
PRIOR REPLICATION NUMBER: US 08/738,000
PRIOR ETLING DATE: 1997-02-12
PRIOR APPLICATION NUMBER: PCT/CA95/00314
PRIOR APPLICATION NUMBER: PCT/CA95/00314
PRIOR APPLICATION NUMBER: GS 9410620.0
PRIOR FILING DATE: 1994-05-25
PRIOR FILING DATE: 1994-05-26
PRIOR FILING DATE: 1994-05-26
NUMBER OF SEO ID NOS: 18
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 2219
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)...(1983)
US-09-931-795-3
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publication No. U320020198211A1
GEMERAL INFORMATION:
APPLICANT: ROZEN, Rima
TITLE OF INVENTION: CDNA FOR HUMAN METHYLENETETRAHYDROFOLATE
TITLE OF INVENTION: ENDUCTASE AND USES THEREOF
FILE REFERENCE: 04844/005003
CURRENT APPLICATION UMBER: U5/09/931,795
CURRENT FILING DATE: 2001-08-16
CURRENT FILING DATE: 2001-08-16
CURRENT FILING DATE: 2001-08-16
                                                                                                                                                                 GCATGCACCGACATGGCCATCACTTGGCCCATCGTCCCGGGATCTTTCCCATCCAGGGC
                                       TyrLysGlyPheIleArgMetThrGlyPheCysLysThrLysIleProAlaAspIleMet
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                  SerLeuValAspAsnAspTyr---IleAsnGlyAspLeuPheAlaValPheAlaAsp 407
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; LOCATION: (13)...(1983)
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SEQ ID NO 3
LENGTH: 2219
TYPE: DNA
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CURRENT FILLING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: US 09/258,928
PRIOR FILLING DATE: 1999-03-01
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APPLICANT: Sekhon, Jaspreet
TITLE OF INVENTION: CDNA FOR HUMAN METHYLENETETRAHYDROFOLATE
TITLE OF INVENTION: REDUCTASE AND USES THEREOF
FILE REFERENCE: 04844/006001
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SOFTWARE: FastSEQ for Windows Version
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SerAspTyrGln---
                                                               TGGGACGAGTTCCCTAACGGCCGCTGGGGCAATTCCTCTTCCCCTGCCTTTGGGGAGCTG
                                                                                                                                              GATGTACGTCCCATCTTCTGGGCCTCCAGACCAAAGAGTTACATCTACCGTACCCAGGAG
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                                                                                      TrpaspGlnTyrProHisGlyArgTrpGlyAspSerCysAsnProSerTyrGlyAlaLeu
                                                                                                                                                                          AspValArgProIlePheTrpAlaAsnArgProLysSerTyrIleSerArgThrIleGly
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1213 AAGGACTACTACCTCTTCTACCTGAAGAGCAAGTCCCCCAAGGAGGAGCTGCTGAAGATG

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TITLE OF INVENTION: COMA FOR HUMAN METHYLENETETAHYDROFOLATE
TITLE OF INVENTION: REDUCTASE AND USES THEREOF
FILE REBERENCE: 04844/005003
CURRENT APPLICATION NUMBER: US/09/931,795
CURRENT FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: US 09/592,595
PRIOR FILING DATE: 2000-06-12
PRIOR FILING DATE: 2000-06-12
PRIOR APPLICATION NUMBER: US 09/258,928
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 08/738,000
PRIOR FILING DATE: 1997-02-12
PRIOR APPLICATION NUMBER: US 08/738,000
PRIOR FILING DATE: 1995-05-25
PRIOR FILING DATE: 1995-05-25
PRIOR FILING DATE: 1995-05-25
PRIOR FILING DATE: 1994-05-26
PRIOR FILING DATE: 1995-05-25
NUMBER OF SED ID NOS: 18
SOFTWARE: FRATSEQ for Windows Version 4.0
LENGTH: 2220
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, Sequence 1, Application US/09931795
, Publication No. US20020198211A1
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ORGANISM: Homo sapiens
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GENERAL INFORMATION

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US-09-728-910-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2220
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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TITLE OF INVENTION: CDNA FOR HUMAN METHYLENETETRAHYDROFOLATE
TITLE OF INVENTION: REDUCTASE AND USES THEREOF
FILE REFERENCE: 04844/006001
CURRENT APPLICATION NUMBER: US/09/728,910
CURRENT FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: US 09/258,928
PRIOR FILING DATE: 1999-03-01
NUMBER OF SEQ ID NOS: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1870 AACCTGGTGGACAATGACTTCCCACTGGACAACTGCCTCTGGCAGGTGGTGGAAGAC 1926
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690 ACTTGGGGCATCTTCCCTGGGCGAGAGATCATCCAGCCCACCGTAGTGGATCCCGTCAGC 174:
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796 TACCACTCCCTTCGGCAGCTTGTGAAGCTGTCCAAGCTGGAGGTGCCACAGGAGATCAAG 855
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                                  TyrLysGlyPheIleArgMetThrGlyPheCysLysThrLysIleProAlaAspIleMet 60
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979.00
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370 ProGluAspGluAlaSerArgLysLeuValGluGluValGlyGlySerHisPheLeuVal 389	P &
350 PheAsnValTrpLysAspGluAlaPheGluIleTrpSerArgGlyTrpAlaSerLeuTyr 369	ОУ
330 ThrTrpG1yVa1PheProAlaLysG1uIleIleGlnProThrIleValAspProValSer 349	Qy Db
310 AlaValAsnLysAspGlySerTrpLysSerAsnValGlyGlnThrAspValAsnAlaVal 329	Db Qy
291 GluLysLeuAspAlaLeuValAspLysCysLysAspArgThrSerLeuThrTyrMet 309      ::     :::     1570 GAGACAGCGGAAGCACTTCTGCAAGTGCTGAAGAAGTACGAGCTCCGGGTTAATTACCAC 162	ОУ
271 TrpGlyGlyProGlyGlyTyrValTyrGlnLysAlaTyrValGluPhePheCysSerLys 290	ρb
251 LeuThrIleAsnSerGlnProAlaValAsnGlyGluLysSerAspSerProThrValGly 270	Ф
231 LeuGlnProGluThrLysIleAleAsnGluGlnLeuGluLysIleAsnThrLysGlyPhe 250	Фр
218 GlyLysLeuArgSerAsn	Ωу
198 TrpAlaValProLeuLysSerValGluAspIleTyrGluArgPheArgLeuTyrCysLeu 217	Qу Db
180 SeraspTyrGlnPheMetArgProArgAlaArgAspLysLysLeuValGluGlu 197	Оу
160 TrpaspGlnTyrProHisGlyArgTrpGlyAspSerCysAsnProSerTyrGlyAlaLeu 179	Qу
140 AspValArgProIlePheTrpAlaAsnArgProLysSerTyrIleSerArgThrIleGly 159 	Дy
120 SerLysValSerArgSerLeuProTrpArgArgProAlaAsnValPheArgValLysGlu 139 	Qу
100 ThrLeuAsnMetGluLysSerAlaLeuAlaIleLeuMetAsnLeuGlyLeuIleGluGlu 119	ОУ
81 GlyThrGluMetCysLysLysIleLeuAlaHisGlyIleLysThrLeuHisLeuTyr 99 	Оy
61 AlaAlaLeuGluProIleLysAspAsnGluGluAlaValLysAlaTyrGlyIleHisLeu 80 	Qy Db

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APPLICANT: Hoffman, Neil
APPLICANT: Hoffman, Neil
APPLICANT: Hurban, Patrick
FITLE OF INVENTION: Expressed Sequences of Arabidopsis
FITLE OF INVENTION: thaliana
FILE REFERENCE: 2023US (PARA-012PRV)
CURRENT APPLICATION NUMBER: US/09/770,445
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: US 60/178,472
PRIOR APPLICATION NUMBER: US 60/178,472
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity:
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SEQ ID NO 690
LENGTH: 832
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                                                                                                                         266
                                                                                                                                                                                                                                                                                                                                          CGTCCGCGAGCACGTGACAAGAAGCTTCAACAAGAATGGGTTGTCCCACTGAAAAGTGTT
LeuThrTyrMetAlaValAsnLysAspGlySerTrpLysSerAsnValGlyGlnThrAsp 325
                                                                                                                                                                   AsnThrLysGlyPheLeuThrIleAsnSerGlnProAlaValAsnGlyGluLysSerAsp 265
                                                                                                                                                                                                                 GAAGATATTCAGGAGAAATTCAAGGAGCTCTGCCTTGGAAACCTTAAAAGCAGTCCCTGG
                                               PhePheCysSerLysGluLysLeuAspAlaLeuValAspLysCysLysAspArgThrSer 305
                                                                                      TTCTTCTGCTCAAAGGAGAAATTAGATGCAGTGGTGGAGAAATGCAAAGCTTTGCCATCG
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Hamilton, Carol M.
Price, Jennifer L.
Raines, Tracy M.
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Kricker, Maja
Slader, Ted
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Woessner, Jeffrey P.
Haas, William David
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Rameaka, Joshua G.
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US-10-113-852A-1
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Best Local Similarity:
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
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APPLICANT: Hanson,
APPLICANT: Raymond,
APPLICANT: Roje, Sa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Biosynthesis of S-Adenosyl Methionine in a Recombinant Yeast FILE REFERENCE: 119927-1033
CURRENT APPLICATION NUMBER: US/10/113,852A
CURRENT FILING DATE: 2002-03-29
PRIOR APPLICATION NUMBER: 60/280,333
PRIOR APPLICATION NUMBER: 60/280,333
PRIOR FILING DATE: 2001-03-30
                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: (826)..(2
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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                               1498
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GluProIleLysAspAsnGluGluAlaValLysAlaTyrGlyIleHisLeuGlyThrGlu
                               TTCTTGAGAAGGATCCAATGGGGCCAAATCTCCATCCCTCAACATTTCTCGTCCCGATTG
                                                     PheIleArgMetThrGlyPheCysLysThrLysIleProAlaAspIleMetAlaAlaLeu
                                                                                            GlnIleGlyIleThrCysProIleValProGlyIleMetProIleAsnAsnTyrLysGly 43
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Hanson, Andrew D.
Raymond, Rhonda R.
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                                                                   GluAspGluAla---SerArgLysLeuValGluGluValGlyGlySerHisPheLeuVal
                                                                                                                                                                       ThrIleAsnSerGlnProAlaValAsnGlyGluLysSerAspSerProThrValGlyTrp
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             SerLeuValAspAsnAspTyrIleAsnGlyAsp 400
                                                                                                                                                                                                               GACTCTCAAGGTGACCTGCTAAGTAATCATCCAGACAACTCCAAGTCCAACGCTGTGACT
                                                                                                                                                                                                                            AsnLysAspGlySerTrpLysSerAsn---ValGlyGlnThrAspValAsnAlaValThr
                                                                                                                                                                                                                                                                  AAGTTGCCCAAGTTGATTGACACCTTGAAAAACAATGAGTTCTTGACCTACTTCGCCATC
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                                                                                                                               AsnValTrpLysAspGluAlaPheGluIleTrpSerArgGlyTrpAlaSerLeuTyrPro
                                                                                                                                                          TGGGGTATTTTCCCCGGCAGAGAAATTCTTCAACCTACCATTGTCGAGAAAATTTCGTTC
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; LOCATION: (1)..(573
; OTHER INFORMATION:
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Best Local Similarity:
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SOFTWARE: PatentIn Ver. 2.1/WordPerfect
SEQ ID NO 61
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APPLICANT: Duwenig, Elke
APPLICANT: Schmidt, Ralf-Michael
APPLICANT: Schmidt, Ralf-Michael
TITLE OF INVENTION: Moss genes from Physcomitrella patens encoding
TITLE OF INVENTION: the
TITLE OF INVENTION: synthesis of amino acids, vitamins, cofactors,
TITLE OF INVENTION: nucleosides
FILE REFERENCE: BASF-NAE-1331-99-US
CURRENT APPLICATION NUMBER: US/09/734,017A
CURRENT FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: 60/171,100
PRIOR FILING DATE: 1999-12-16
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TYPE: DNA
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                                                                                                                                                                                 GluMetCysLysIjeLeuAlaHisGlyIleLysThrLeuHisLeuTyrThrLeuAsn 102
                                                                                                                                                                                                                                                     LeuGluProIleLysAspAsnGluGluAlaValLysAlaTyrGlyIleHisLeuGlyThr
                                                                                                                                                                                                                                                                                                                                    GlyPheIleArgMetThrGlyPheCysLysThrLysIleProAlaAspIleMetAlaAla
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                                                    SerArgSerLeuProTrpArgArgProAlaAsnValPheArgValLysGluAspValArg
                                                                                                                                  MetGluLysSerAlaLeuAlaIleLeuMetAsnLeuGlyLeuIleGluGluSerLysVal
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ProIlePheTrpAlaAsnArgProLysSerTyrIleSerArgThrIleGlyTrpAspGln
                                 TCTCGTCCTCTACCGTGGAGGCCTCCAACTAACAGCAAGCGTACAAAGGAGGACGTGCGT
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Ehrhardt, Thomas
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Best Local Similarity:
Query Match:
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; ORGANISM: Glycine max
; OTHER INFORMATION: Clone
US-09-878-574-3765
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)8
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 3765
LENGTH: 313
GENERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Kamigoaki, Laura Y. (Ito)
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
                                                                             Sequence 5596, Application US/09923876 Patent No. US20020013958A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3765, Application Patent No. US20020110548A1 GENERAL INFORMATION:
                                                                                                                                                       241
                                                                                                                                                                  402 PheAlaValPheAla 406
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                                                                                                                                                    TTTGCCGTCTTTGCA
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CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 09/298,329
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/085,331
PRIOR APPLICATION NUMBER: 60/085,331
PRIOR FILING DATE: 1998-05-05
NUMBER OF SEQ ID NOS: 6332
                                                                                                                                                                                                                                                                                                Sequence 476, Application US/09923876 Patent No. US20020013958A1 GENERAL INFORMATION:
                  SOFTWARE: PERL Program
SEQ ID NO 476
LENGTH: 265
TYPE: DNA
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                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/923,876
CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 09/298,329
PRIOR FILING DATE: 1999-04-21
                                                                                                                                                                                                            APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Kamigaki, Laura Y. (Ito)
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
FILE REFERENCE: PL-0012-1 CON
                                                                                      PRIOR APPLICATION NUMBER: 60/085,331
PRIOR FILING DATE: 1998-05-05
NUMBER OF SEQ ID NOS: 6332
ORGANISM: Zea mays
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OTHER INFORMATION: Inc:
NAME/KEY: unsure
LOCATION: 81, 183
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ORGANISM: Zea
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11-AUG-1999; 12-AUG-1999; 13-AUG-1999;

99US-0148319. 99US-0148341. 99US-0148565.

99US-0148684

99US-0149368. 99US-0149175. 99US-0149426. 99US-0149722.

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99US-0149929.
99US-0149902.
99US-0149930.
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99US-0151065.
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99US-0161993.
99US-0162142.
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99US-0161406.
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99US-0161361.
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99US-0160980
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                                    Score 1184; DB 21;
Pred. No. 9.7e-110;
8; Mismatches 29;
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Conservative

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RESULT 14
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                                                                                                                                                                                                                                                                                                                                      Human methylene:tetra:hydro:folate reductase cDNA probe - for detection of sequence abnormalities in methylene:tetra:hydro:folate reductase e.g. in cardiovascular, neurological or folic acid metabolism disorders
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N-PSDB; AAT09689.
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                                                                                                     Sequence
                                                                                                                                                    This is the protein sequence encoding human MTHFR, the gene of which has been localised to chromosome 1p56.3. Deficiencies of this protein may lead to cardiovascular and neurological disorders and disorders influences by folic acid metabolism.
                                                                                                                                                                                                                                                                                     Disclosure; Fig.6A-6C;
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Score 979; DB 1
Pred. No. 6e-89;
9; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; methylenetetrahydrofolate reductase; MTHFR; gene therapy; glioma; antisense therapy; EC 1.5.1.20; chromosome 1p36.3; cancer; kidney cell; pancreas; lung; brain; cytostatic; colon carcinoma; breast; colorectal; neuroblastoma; leukaemia.
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                                                                                            SDYQ--FMRPRARDKKLVEEWAVPLKSVEDIYERFRLYCLGKLRSN-----PWSELDG 230
                                                                                                                                                                             EKLDALVDKCKD-RTSLTYMAVNKDGSWKSNVGQTDVNAVTWGVFPAKEIIQPTIVDPVS 349
                                                                                                                                                                                                                                         120 SKVSRSLPWRRPANVFRVKEDVRPIFWANRPKSYISRTIGWDQYPHGRWGDSCNPSYGAL 179
                                                   401 KDYYLFYLKSKSPKEELLKMWGEELTSEASVFEVFVLYLSGEPNRNGHKVTCLPWND-EP 459
                                                                                                                                                         231 LOPETKIINEQLEKINTKGFLTINSQPAVNGEKSDSPTVGWGGPGGYVYQKAYVEFFCSK 290
DVIEPIKDNDAAIRNYGIELAVSLCQELLASGLVPGLHFYTLNREMATTEVLKRLGMWTE 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antisense nucleic acids, which are methylenetetrahydrofolate reductase inhibitors, useful for treating, stabilizing or preventing cancer, e.g. breast carcinoma, colon carcinoma, colorectal carcinoma neuroblastoma
                                                                                                                                                                                                                                                                                                      FNVWKDEAFEIWSRGWASLYPEDEASRKLVEEVGGSHFLVSLVDNDY-INGDLFAVFAD 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human methylenetetrahydrofolate reductase (MTHFR) protein #2.
                                                                                                                                                                                                                                                                                                                                                                                               AAE12607 standard; Protein; 656 AA.
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(SEKH/) SEKHON J.
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AAE12607
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neuroblastoma, glioma and leukaemia. MTHFR cDNA probe is used in gene therapy. The present sequence is human methylenetetrahydrofolate reductase (MTHFR) protein #2. Human MTHFR gene is mapped to chromosome 1p36.3.
                                                                                                                                                                                                                                                                                                                                      61 AALEPIKDNEEAVKAYGIHLGTEMCKKILAHG-IKTLHLYTLNMEKSALAILMNLGLIEE 119
                                                                                                                                                                                                                                                                                                                                                                      OVIEPIKDNDAAIRNYGIELAVSLQBELLASGLVPGLHFYTLNREMATTEVLKRLGMWTE 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SKVSRSLPWRRPANVFRVKEDVRPIFWANRPKSYISRTIGWDQYPHGRWGDSCNPSYGAL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 SDYQ--FMRPRARDKKLVEEWAVPLKSVEDIYERFRLYCLGKLRSN-----PWSELDG 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LQPETKIINEQLEKINTKGFLTINSQPAVNGEKSDSPTVGWGGPGGYVYQKAYVEFFCSK 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EKLDALVDKCKD-RTSLTYMAVNKDGSWKSNVGQTDVNAVTWGVFPAKEIIQPTIVDPVS 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44.8%; Score 979; DB 22; Length 656;
44.9%; Pred. No. 6e-89;
ive 79; Mismatches 138; Indels 14; Gaps
                                                                                                                                                                                                                                               1 ARVIVIQLEYDIDIFLKEVNDCRQIGITCPIVPGIMPINNYKGFIRMIGFCKTKIPADIM 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       350 FNVWKDEAFEIWSRGWASLYPEDEASRKLVEEVGGSHFLVSLVDNDY-INGDLFAVFAD 407
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                                                                                                                                                                              Similarity
                                                                                                            656 AA;
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Best Local Simi
Matches 188;
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APPLICANT: Kanigaki, Laura Y. (Ito)
APPLICANT: Kanigaki, Laura Y. (Ito)
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYMUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
FILE REFERENCE: PL-0012-1 CON
CURRENT APPLICATION NUMBER: US/09/923,876
CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 09/298,329
PRIOR APPLICATION NUMBER: 09/298,329
PRIOR APPLICATION NUMBER: 09/298,329
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 09/298,331
PRIOR FILING DATE: 1998-05-05
NUMBER OF SEQ ID NOS: 6332
SOFTMARE: PERL PROGram
SEQ ID NO 5753
LENGTH: 181
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAMEY OF SEC TO FEATURE
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Best Local Similarity:
Query Match:
                                                                                                                                             ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID
; NAME/KEY: unsure
; LOCATION: 2, 165, 173, 180
; OTHER INFORMATION: a, t, c, 9
US-09-923-876-5753
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; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID
US-09-923-876-476
                   Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           218 GlyLysLeuArgSerAsnProTrpSerGluLeuAspGlyLeuGlnProGluThrLys1le
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Conservative:
Mismatches:
Indels:
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            RESULT 14
US-09-294-093B-4653
; Sequence 4653, Application
; Patent No. US20010051335A1
; GENERAL INFORMATION:
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Best Local Similarity:
Query Match:
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; OTHER INFORMATION: Incyte ID No. US20020013958A1 700158929H1
US-09-923-876-1503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 6332
SOFTWARE: PERL PROGRAM
SEQ ID NO 1503
LENGTH: 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1503, Application Patent No. US20020013958A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Kamigaki, Laura Y. (Ito)
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED
FILE REFERENCE: PL-0012-1 CON
CURRENT APPLICATION NUMBER: U5/09/923,876
CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 09/298,329
PRIOR APPLICATION NUMBER: 09/298,329
PRIOR PILING DATE: 1999-04-21
PRIOR FILING DATE: 1999-04-21
PRIOR FILING DATE: 1998-05-05
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Zea mays FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
                                                                                                            121
                                                                                                                                                                                                                                                            294 AspAlaLeuValAspLysCysLysAspArgThrSerLeuThrTyrMetAlaValAsnLys 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 ArgThrileGlyTrpAspGlnTyrProHisGlyArgTrpGlyAspSerCysAsnPro 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  274 ProGlyGlyTyrValTyrGlnLysAlaTyrValGluPhePheCysSerLysGluLysLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 AGGACATTAGGTTGGGATCAGTATCCCCATGGACGGTGGGGTNATTCTCGNAACCCT 179
                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                         1 CCTGGAGGCTACGTTTATCAGAAGGCCTACCTCGAATTCTTCTGCGCAAAGGAGAAGTTG
                                                                                                                                                                             GATGGAGAAACATTCTCCAATATTTCACCGAACGCCGTGAATGCTGTCACGTGGGGTGTT
                                                                                                                                                                                                AspGlySerTrpLysSerAsnValGlyGlnThrAspValAsnAlaValThrTrpGlyVal 333
                                                                                                                                                                                                                                          GACCAACTAATTGAGAAGATCAAAGCATTCCCTTCTCTCACTTACATTGCTGTGAACAAG
 Lalgudi, Raghunath, V
                                                                                                                                                                                                                                                                                                                                                                                                   1.46e-23
274.00
81.69%
71.83%
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                                               US/09294093B
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Matches:
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216 51 7 13 0

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GENERAL LAWLOWASILOW:
APPLICANT: Lerchl, Jens
APPLICANT: Rerchl, Jens
APPLICANT: Reindl, Andreas
APPLICANT: Reindl, Andreas
APPLICANT: Freindrich
APPLICANT: Frank, Markus
APPLICANT: Schmidt, Ralf-Michael
ITILE OF INVENTION: Moss genes from Physcomitrella patens encoding proteins involved
ITILE OF INVENTION: Synthesis of amino acids, vitamins, cofactors, nucleotides and
ITILE OF INVENTION: Nucleosides
ITILE OF INVENTION WHABER: US/09/734,017A
CURRENT APPLICATION NUMBER: US/09/734,017A
CURRENT APPLICATION NUMBER: US/09/734,017A
CURRENT APPLICATION NUMBER: US/09/734,017A
CURRENT FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: US/09/734,017A
SOFTWARE: Patentin Ver. 2.1/WordPerfect
SOFTWARE: Patentin Ver. 2.1/WordPerfect
SOFTWARE: Number of the patentin Ver. 2.1/WordPerfect
SOFTWARE: Number of the patentin Ver. 2.1/WordPerfect
TYDE: DANA
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SOFTMARE:

PERL Program

SEQ ID NO 4653

LENGTH: 159

TYPE: DNA

ORGANISM: Zea mays

FEATURE:

NAME/KEY: misc_feature

OTHER INFORMATION: Incyte ID NO
NAME/KEY: unsure

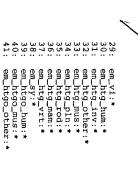
LOCATION: 14

COTHER INFORMATION: a, t, c, g,

US-09-294-093B-4653
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US-09-734-017A-63
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APPLICANT: Sherman, Bradley, K.
APPLICANT: Sherman, Bradley, K.
TITLE OF INVENTION: POLYUNCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
FILE REFERENCE: PL-0009 US
CURRENT APPLICATION NUMBER: US/09/294,093B
CURRENT FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: 60/082,567
PRIOR APPLICATION WIMBER: 60/082,567
PRIOR FILING DATE: APril 21, 1998
NUMBER OF SEQ ID NOS: 6207
SOPTMARE: PERL PROGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                133 AsnValPheArgValLysGluAspValArgProllePheTrpAlaAsnArgProLysSer
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255.00
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Search completed: February 12, 2003, 17:07:24 Job time : 93 secs
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LOCATION: (2)..(409)
OTHER INFORMATION: 62_mm20_cl0rev
                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Physcomitrella FEATURE:
                                                  380
                                                                                                    320 CGTCAAATTGGTATCAAGGTGCCCATTGTACCTGGTATCATGCCCATTCAAAATTACAAG 379
                                                                                                                                                      260 GTCATTATCACCCAGCTGTTTTATGATACCGATATCTTTTTGAAATTTGTGAATGATTGT
                                               23 ArgGlnIleGlyIleThrCysProIleValProGlyIleMetProIleAsnAsnTyrLys 42
                                                                                                                                                                 3 VallleValThrGlnLeuPheTyrAspThrAspIlePheLeuLysPheValAsnAspCys
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Matches:
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Indels:
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                        Database :
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1 ARVIVTQLFYDTDT1
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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2054640 seqs, 14551402878 residues
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Isolation, characterization, and functional expression of concoding NADH-dependent methylenetetrahydrofolate reductase
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Arabidopsis thaliana
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IGENGLASHAYQSLESYLKKKIDAGADLIVTQLFYDTDİFİKFVNDCRQIGISCEPIV
PGIMPINNYRGFIRMTGFCKTKIPVEVMAALEFIKDNEBAYKAYĞIHLGTEMCKKMLA
HGVKSJHİYTLMNEKSALAILMNLGMIDESKISRSLPWRRPANDKTQTEMDVRPIFWAN
RPKSYISRTKGMEDFPQGRWGDSRSASYGALSDHQFSRPARDKKLQQEVVPLKYE
DIQEKFKELCLGKLKSSEWSELDGLQFETRIINSQLIKVNSKGFLTINSQPSVNAERS
DSPTVGWGGPYGYVYQKAYLEFFCSKEKLDAVVEKCKALPSITYMAVKKGEQWVSNTA
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/proteln_id="AAD55788.1"
/db_xref="g1:5911427"
/translation="MKVIDKIQSLADEGKTAFSFEFFPPKTEDGVDNLFERMDRMVAY
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                                                                                       TrpSerArgGlyTrpAlaSerLeuTyrProGluAspGluAlaSerArgLysLeuValGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shinn, P. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equall this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (02-AUG-2001) Salk Institute Genomic Analysis Laboratory (SIGNAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AY050434.1 GI:15215809 FLI_CDNA.
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/protein_id="AAK91450.1"
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                                                                                                                                                                                                                                                                                                                            /clone="RAFL05-16-121(R13348)"
/note="ecotype: Columbia"
                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                 /note="putative methylenetetrahydrofolate
                                                                                                                                                                                                                                                                                                                                                                                                    /chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
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GlnLeuGluLysIleAsnThrLysGlyPheLeuThrIleAsnSerGlnProAlaValAsn
                                                                                                          ProLeuLysSerValGluAspILeTyrGluArgPheArgLeuTyrCysLeuGlyLysLeu
                                                                                                                                                         GATCATCAGTTCTCACGTCCGCGAGCACGTGACAAGAAGCTTCAACAAGAATGGGTTGTC
                                                                                                                                                                        AspTyrGlnPheMetArgProArgAlaArgAspLysLysLeuValGluGluTrpAlaVal
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                            GTGCGCCCCATTTTCTGGGCAAACCGTCCAAAGAGCTACATTTCTAGAACCAAGGGCTGG
                                                                                          CCACTGAAAAGTGTTGAAGATATTCAGGAGAAATTCAAGGAGCTCTGCCTTGGAAACCTT
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IGENGLASNEAYOSDLEYLKKKIDAGADLIVTQLFYDTDIFLKEVNDCROIGISCPIV
PGIMPINNYRGFLRMTGFCKTKIPVETWAALBEIKNDEAYGAYGIHLGTEXDKYKHA
HGYKSLHLYTLNMEKSALAILMNIGMIDESKISRSLPWRRPANVFRTKEDVRPIFWAN
RPKSYISRTKGWEDFPQCRWGDSRSASYGALSDHOFSRPARDXKLQOGWVVPLKSVE
DIQEKFKELCLGNLKSSPWSELDGLQPETRIINEQLIKVNSKGFLTINSQPSVNAERS
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OADVNATTWGVFPAKEIIQPTIVDPASSNVKDEAFETWSRSWANLYPEADPSRNLLE
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1 (bases 1 to 2034)

Southwick, A., Karlin-Neumann, G., Nguyen, M., Lam, B., Miranda, M., Palm, C.J., Bowser, L., Jones, T., Banh, J., Carninci, P., Chen, H., Cheuk, R., Chung, M.K., Hayashizaki, Y., Ishida, J., Kamiya, A., Kawai, J., Kim, C., Lin, J., Liu, S.X., Narusaka, M., Pham, P.K., Sakurai, T., Satou, M., Seki, M., Shinn, P., Yamada, K., Shinnozaki, K., Ecker, J., Theologis, A. and Davis, R.W.
                 The Salk, Stanford, PGEC (SSP) Consortium members carried out sequencing and annotation of the RAFI CONAS: Southwick,A., Karlin-Neumann,G., Nguyen,M., Lam,B., Miranda,M., Palm,C.J., Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R., Chung,M.K., Kim,C., Lin,J., Liu,S.X., Pham,P.K., Sakano,H., Shinn,P., Yamada,K., Ecker,J., Theologis,A. and Davis,R.W.
                                                                                                                                                 RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFI cDNAs (RAFI cDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J. Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (17-APR-2001) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                                                                              correspondence:
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Southwick, A. (SSP/Stanford) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Davis, R.W. (SSP/Stanford) contributed equally to this work as PIs. Location/Qualifiers
/note="This clone is in pBluescript
ecotype: Columbia"
                                                                                                                                                                                                                                                                                                                                      /organism="Arabidopsis/db_xref="taxon:3702"
                                                                                                                                                                                                                         /gene="At2g44160; F6E13.29"
                                                                                                                                                                                                                                                                                                            /clone="RAFL11-04-D03"
                                                                                                                                                                                                                                                     "At2g44160; F6E13.29"
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1.46e-152 1834.00 91.15% 82.06% 83.86% Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 2034 334 37 36 0

US-09-720-451-6 (1-408) x AF370515 (1-2034)

LysValSerArgSerLeuProTrpArgArgProAlaAsnValPheArgValLysGluAsp 140 LeuAsnMetGluLysSerAlaLeuAlaIleLeuMetAsnLeuGlyLeuIleGluGluSer 120 GlyThrGluMetCysLysIleLeuAlaHisGlyIleLysThrLeuHisLeuTyrThr 100 AlaAlaLeuGluProIleLysAspAsnGluGluAlaValLysAlaTyrGlyIleHisLeu GATTGTCGGCAAATTGGGATTAGTTGTCCCATTGTTCCTGGAATTATGCCTATTAATAAC AspCysArgGlnIleGlyIleThrCysProIleValProGlyIleMetProIleAsnAsn 40 GGAACAGAGATGTGTAAAAAGATGTTGGCTCATGGAGTCAAGTCTCTTCATCTCTACACA GCTGCCTTGGAGCCTATCAAGGATAACGAAGAAGCTGTGAAAGCCTATGGTATTCACCTT 1008 160 948 80 888 828 60

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RESULT 4
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AJ245414 AJ245414.1 GI:5823582
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
Rosidae; eurosids II; Brassicales; Brassicaceae; Arab
I (bases I to 2037)
Ravanel, S., Rebeille, F. and Douce, R.
Folate metabolism in higher plants: cloning of a cDNA
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Direct Submission
Submitted (27-JUL-1999) Ravanel S., Di
CEA-Grenoble, 17, rue des Martyrs, 38
Location/Qualifiers
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ValargProIlePheTrpAlaAsnArgProLySSerTyrIleSerArgThrIleGlyTrp 160
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GENGLASNEAVQSDLFYLKKKIDAGADLIVTOLFYDTDIFLKFVNDCRQIGISCFIV
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GENGLASNEAVQSDLEYLKKKIDAGADLIVTOLFYDTDIFLKFVNDCRQIGISCFIV
PGIMPINNYRGFLAMTGFCKTKIPVETWAALEBIKDNEEAVRAYGHILGTEMCKKMLA
HGVKSLHLYTINMEKSALAILMNLGMIDESKISRSLPARDKKLQOEMVVPLKSVE
PGIMPINNYRGFPAGNEBDSRASYGALSDHQFESRPARDKKLQOEMVVPLKSVE
DIQEKFKELCIGNLKSSPMSELDGLQPETRIINEQLIKVNSKGFLTINSOPSVNAERS
DSPTVGWGGFVGVVCKAYLEFFCSKEKLDAVVEKCKALPSITYMANNKGEGWVSNTV
QADVNAVTMQVFPAKAEIIQPTIVDPASENWKDEAFETWSRSWANLYPEADPSRNLLE
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/codon_start=1
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68. .1852
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/db_xref="taxon:3702"
68. .1852
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/EC_number="1.5.1.20"
/function="reduction
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Southwick, A.,

Hsuan, V.W.,

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AUTHORS
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The RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., ishida, Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai, J., Hayashizaki,Y. and Shinozaki,K.
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Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.
Arabidopsis Open Reading Frame (ORF) Clones
Unpublished
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/db_xref="GI:21689667"
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/db_xref="taxon:3702"
/chromosome="3"
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(RIKEN GSC) and Theologis, A. (SSP
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GlnProThrIleValAspProValSerPheAsnValTrpLysAspGluAlaPheGluIle
                                                                                                                                                             GlyGluLysSerAspSerProThrValGlyTrpGlyGlyProGlyGlyflyTyrValTyrGln
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                              ACCGGTGAGTCCGATGTGAATGCAGTTACTTGGGGAGTGTTCCCAGCTAAGGAGGTTATT
                                        ValGlyGlnThrAspValAsnAlaValThrTrpGlyValPheProAlaLysGluIleIle
                                                                                                          CCACTGAAAAGCATTGAAGATGTTCAAGAGAATTCAAAGAGCTCTGCATTGGAAACTTA
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                                           Scores:
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Submitted (31-AUG-1999) Horticultural Sciences,
Submitted (31-AUG-1999) Horticultural Sciences,
Florida, Hull Road, Gainesville, FL 32611-0690,
Florida, Jocation/Qualifiers
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Augnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 1994)
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Roje, S. and Hanson, A.D.
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eptfcdtwgaggstadlfletasrmdrucvenmhltgtnnptektenterndrusy
eptfcdtwgaggstadlfletasrmdrucvenmhltgtnnptektenthaleftrsn
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pgimpisnykgflrmagfcktkifpaeltaalepikdndeavkaygiffatemckkila
hgitslhlytlnvdksalgilmniglidbskisstyfrarparvarfkedvrfikedvrfikerparparvarfksylfshytlnvdksalgilmniglidbskisstygfarrkgdkklogvvolksie
pvobkfkelcignlksspaseldglopefyiinbglkinsgfftinsopsvnaaks
dspalgagggggvygkayleffcskokldtlkekskapsitmavaksbendkvitg
byalgagggggygygkayleffcskokldtlkekskapsitmavaksbendkvitg
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5-methyltetrahydrofolate (CH3-THF)
/note="NADH-dependent"
/codon caca1yzes the reduction of
/note="NADH-dependent"
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EVKNSYYLVSLVDNNYINGDIFSVFA"
1 404 c 455 g 575 t
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/protein_id="AAD55787.1"
/db_xref="GI:5911425"
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γ	P &	P 40	₽ <b>2</b> 4	Qy Db 1	D V	Db Qy	Db Qy	D	₽ <b>Q</b>	g So	Dy Oy	Дy	Db Qy	Dy VQ	Qy Db	ОУ	US-09	Percen Best L Query DB:
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ValGlyGlnThrAspValAsnAlaV	LysaspargThrSerLeuThrTyrMo         aaaGCTTTTCCTTCTTATCACCTACAC	LysalaTyrValGluPhePheCysSo             AAAGCTTATCTGGAGTTCTTCTGTT	GlyGluLysSerAspSerProThrVa               GCAGCCAAATCCGATTCTCCAGCTAT	GlnLeuGluLysIleAsnThrLysG                :::    CAACTCGGAAAAATCAACTCCAACGC	ArgSerAsnProTrpSerGluLeuA: :::   :::	ProLeuLysSerValGluaspIleTy         :::  CCACTGAAAAGCATTGAAGATGTTCJ	AspTyrGlnPheMetArgProArgAli            GATTATCAGTTTGCGCGCCCAAAAGG	AspGlnTyrProHisGlyArgTrpG: ::: :::	ValargProllePheTrpAlaAsnA: 	LysValSerArgSerLeuProTrpAr    :::                  AAAFTTCTCGTTCTCTACCTTGGAG	LeuasnmetGluLysSeralaLeua)        ::::  TGAACGTGGACAAATCAGCTATTG	GlyThrGlumetCysLysLysIleL6                CaaCAGAAATGTGCAAAAAGATTTT	AlaAlaLeuGluProIleLysAspAs 	TyrLysGlyPheIleArgMetThrGl                  TACAAGGGGTTCTTGCGTATGGCTGC	AspCysArgGlnIleGlyIleThrCy                    GATTGTCGGCAAATCGGGATTAATTG	AlaArgVallleValThrGlnLeuPhe	451-6 (1-408) x AF181966 (	milarity: 89.418 Similarity: 78.578 h: 81.25%
AlavalThrTrpGlyValPhePr	etAlavalAsnLysAspGl                 TGGCCGTGAACAATCAGA	erLysGluLysLeuAspAl       :::          CAAAGGATAAGTTAGACAC	lGlyTrpGlyGlyProGl :           TGGATGGGGTGGTCCTGC	lyPheLeuThrIleAsnSe 	spGlyLeuGlnProGluTh 	YrGluargPheArgLeuTyr     :::    :::  AAGAGAAATTCAAAGAGCTC	aArgAspLysLysLeuVa           cgrgacaagaagcttca	lyAspSerCysAsnProSe           stgatTCACACAGTGCAGC	rgProLysSerTyrIleSe 	gArgProAlaAsnValPh              acgccrgcaaargrrr	laIleLeuMetAsnLeuGl              GGATATTAATGAACCTTGG	.euAlaHiSGlyIleLySTh             ::  TGGCCCATGGAATCACTTC	nGluGluAlaValLys <i>P</i>  :::             TGACGAGGCTGTTAAAC	lyPheCysLysThrLysIle 	SProlleValProgly             CCCATTGTTCCTGG	TYTASPThrASPILEP 	(1-1994)	Conservative: Mismatches: Indels: Gaps:
coAlaLysGluIleIle	lySerTrpLysSerAsn :::            AGAATTGGGTATCAAAC	aLeuValAspLysCys       :::    !ACTTGTGGAGAAATCC	.yGlyTyrValTyrGln             rggTTACGTCTACCAG	rGlnProAlaValasn       ::::       CCAACCATCAGTCAAT	rLysIleIleAsnGlu            AAAGATCATAAATGAG	rCysLeuGlyLysLeu     :::     CTGCATTGGAAACTTA	alGluGluTrpAlaVal :::      AGCAAGAATGGGTCGTC	erTyrGlyAlaLeuSer ::     CATACAGTACACTTTCG	erArgThrIleGlyTrp          cTAGAACAAAGGGCTGG	neArgValLysGluAsp        CCGTACTAAGGAAGAT	YLeuIleGluGluSer       :::       TCTGATTGATGAGTCA	hrLeuHisLeuTyrThr ::            CCCTTCATCTCTACACA	laTyrGlyIleHisLeu             CCTATGGAATTCACTTT	eProAlaAspIleMet        :::::  ACCCGCTGAGCTCACT	VIleMetProIleAsnAsn               ATTATGCCTATTTCCAAC	heLeuLysPheValAsn            rccrcaagriigtgaar		44 43 0
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TITLE
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E 1 (bases 1 to 2002)

S Yamada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Chung, M.K., Goldsmith, A.D., Lee, J.M., Quach, H.L., Toriumi, M., Yu, G., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A. Arabidopsis Full Length cDNA Clones

[In Davis, R. W., Ecker, J.R. and Theologis, A. Arabidopsis Full Length cDNA Clones

[In Davis, R. W., Ecker, J.R. and Theologis, A. Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, K., Shinozaki, Shinozaki, K., Shinozaki, K., Shinozaki, Shinozaki, K., Shinozaki, Shinozaki, Shinozaki, Shinozaki, Shinozaki, Shinozaki, Shinozaki, Shinozaki, Shinozaki, Shinozaki, Shin
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                                                                                                                                                                                                               The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RaFI cDNAs: Yamada,K., Banh,J., Chang,C.H., Chang,E., Dale,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Yu,S., Bowser,L., Chen,H., Cheuk,R., Jones,T., Karlin-Neumann,G., Kim,C., Lam,B., Lin,J., Meyers,M.C., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R. and Theologis,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (12-DEC-2001) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA
RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFI cDNAs (RAFI cDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
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Yamada,K., Banh,J., Chang,C.H., Chang,E., Dale,J.M.,
Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C.,
Goldsmith,A.D., Lee,J.M., Onodera,C.S., Yu,S., Bowser,L.,
Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Yu,S., Bowser,L.,
Carninci,P., Chen,H., Cheuk,R., Hayashlzaki,Y., Ishida,J.,
Jones,T., Kamiya,A., Karlin-Neumann,G., Xim,C., Liam,B.,
Lin,J., Meyers,M.C., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J.,
Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A.,
Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.
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Yamada,K. (SSP/PGEC) and Seki,M. (RIKEN GSC) contributed equally to
this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGEC)
contributed equally to this work as PIs.
Location/Qualifiers
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clade; Panicoideae; Andropogoneae; Zea.

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Embryophyta; Tracheophyta; a; Poales; Poaceae; PACC

KEYWORDS

AF174486.

GI:5802605

REFERENCE

TITLE AUTHORS

Roje, S., Wang, H., McNeil, S.D., Raymond, R.K., Appling, D.R., Shachar-Hill, Y., Bohnert, H.J. and Hanson, A.D. Isolation, characterization, and functional expression of cDNAs encoding NADH-dependent methylenetetrahydrofolate reductase from

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PNAVNAVTWGVEPGKEIIQPTVVDHASFMYWKDEAFEIWTRGWGCMFPEGDSSRELLE
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Arabidopsis thaliana chromosome 2 clone F6E13 map CIC10F02,
CIC10ZE07, complete sequence.

NACO04005

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ACO04005.3 GI:20197067

S HTG.

Arabidopsis thaliana.

Arabidopsis thaliana.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; streptophyta; Embryophyta; Arabidopsis.

Eukaryota; Viridiplantae; Brassicaceae; Arabidopsis.

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

E 1 (bases 1 to 10974)

Rounsley,S.D., Kaul,S., Lin,X., Ketchum,K.A., Crosby,M.L.,
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|||:::|||||||
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                                                                                                                                                                                                                             CTGTTTGCTGCCTTC
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2 (bases 1
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Location/Qualifiers
1. .109741
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gene="AL2943880"
                                                                                                                                     complement(9101.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="F6E13.2"
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                                                                                                                                 .14090)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .8032,8122. .8350,8440. .8658)
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complement(14748. .17292)
/gene="At2g43910"
                                                                                                                                                                                                                                                                                                                                  /rpt_family="AT_rich"
17774 .17794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(14925. 15617. .15716,15874. .1 17119. .17218))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(join(<14748. .14963,15285. .15363,15476. .15522, 15617. .15716,15874. .15974,16059. .16145,16677. .16807,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ceres:24370"
       complement(join(<19342. .19624,19773. .19851,19988. .200
20130. .20229,20308. .20408,20521. .20607,20828. .20958,
                                                                                                  /rpt_family="AT_rich" complement(19342. .21515) /gene="At2g43920"
                                                                                                                                                                                                                                                                                                                                                                                                                /rpt_family="AT_rich" complement(17642. .170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="AT_rich"
complement(16570. .16
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KANETYGSSPKAEYFSFVKEDVFTWRPTELFDLIFDYVFFCAIEPEMRPAWAKSMYEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="At2g43910"
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/protein_id="AAC23400.1"
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                                                                         /note="F6E13
                                                                                                                                                                                                               /rpt_famil
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LKPDGELITLMYPITDHVGGPPYKVDVSTFEEVLVPIGFKAVSVEENPHAIPTRKGKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="GI:3212849"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=
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.15974,16059. .16145,16677. .:
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.16807 .15522,

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DYLHOPE GEBEOFQLEEFYGSGGGGVGKEV PFINSPLEEF FAR I LINDSEF FAR IN TELLY SOCIAL SOLDER FERRITACTER PHELKERGVGR

FERRITACTEROLIMAGOESGVERWINDDAFERGCGLSGRVGROEDAAPROESASTSPT
TCLMVDNGNRLVWSGHKDGKIRSWKDYVLDDGDDSPFKEGLAWDAKGPVNSVIMSS
YGDLMSGSEGGVIKINTWESSEKKSLSLELEEKHMAALLVERSGLDLRACVTVNGTCNI
SSSEYKCLLADNVRSKVWAAQLOTESLWDGRTXELLKVRSEGGTENRVDMFJGQDQP
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DTFYLRITNKCVKENAVFRILCEGGSTVREDEDTLELHPLGSFGFPRWLEVMPAAGTI
KPDSSYEVSVHHEEFHTLEEFYDGIPOONWCEDTREKERT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="unknown protein"
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LKPDGELITLMYPMTDHEGGAPYKVALSSYEDVLVPVGFKAVSVEENPDSIPTRKGKE
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32	eArgLeuTyrCysLeuGlyLysLeuArgSerAsnProTrpSerGluLeuAspGlyLeuGl 2  :::	212	Qy
14669	CAGAAATT 9	94610	Db
212	Ph 2	211	Qy
4609	   GAGGTAGAACAATTTTTTCACTACCACACATTTCCCTCACTTTCA 9	94550	Db
019	112	205	Qy
204 94549	TCACGTCCGCGAGCACGTGACAAGAAGCTTCAACAAGAATGGGTTGTCCCACTGAAAAGT	94490	90 72
	TADATGTAACATCTTCTTGTGAGCTTGTTTGCTGAACTAAATGCTTTTGTTGTCAGTTC	oω	) B
184		18	Qy
94429	ATAACAAAGGGGTTTTGAAGGGTATTTCTTCGATTGGTCTTTTTGATTTGCTCTAGATTG 9	94370	DЬ
182	1	182	Qy
94369	TCGGATCATCAGGTACTACAATACATCATCTGTAATTGCACAACTCTCTTTCAAGATTTC 9	94310	Db
182	SerAspTyr1	180	Qy
94309	CAGT	94250	DЪ
179	spGlnTyrProHisGlyArgTrpGlyAspSerCysAsnProSerTyrGlyAlaLe	160	Qy
94249	TITCTICIAATCITTGAAGGGCAAACCGTCCAAAGAGCTACATTTCTAGAACCAAGGGC 9	94190	DЪ
159	aAsnArgProLysSerTyrIleSerArgThrIleGly	147	Qy
94189	CTCTCGTTCTGATTATACTTAGCCACATATTTTACTCTGCAGGGAAAATAAGACTTGTTC ;	94130	Db
146		146	Qy
94129	CAPATGTTTTCCGTACTAAGGAAGATGTGCGCCCCATTTTCTGGTAACAGAGCTTAGTTT :	94070	Db
146	lLysGluAspValArgProIlePheTrp	132	Qy
4	AGAATCTTGGTATGATTGATGAGTCCAAAATTTCTCGTTCTTTACCCTGGAGACGCCCTG	94010	Дb
132	AsnLeuGlyLeuIleGluGluSerLysValSerArgSerLeuProTrpArgArgProA	113	Qy
94009	CTACTTGATGTAAAGCATGATACTGATAGTGGAGTAGCTTTACTATTTTGTTGTTGTTTTC !	93950	Db
112		112	Qy
93949	CTACACATTGAACATGGAGAAATCTGCTCTTGCAATATTGATGGTTGGT	93890	Дδ
112	GluLysSerAlaLeuAlaIleLeuMet	98	Qy
93889	TCACCTTGGAACAGAGATGTGTAAAAAGATGTTGGCTCATGGAGTCAAGTCTCTTCATCT	93830	DЬ
98	HisLeuGlyThrGluMetCysLysLysTleLeuAlaHisGlyTleLysThrLeuHisLe	78	Qy
93829	GGTGATGCCTTGGAGCCTATCAAGGATAACGAAGAAGCTGTGAAAGCCTATGGTAT	93770	Дb
78	pīleMetAlaAlaLeuGluProīleLysAspAsnGluGluAlaValLysAlaTyrGlyIl	58	Qy
	TTTTGTGAAAAAAGATAGATGAATTTACATATGATTATATTAATGTAGATACCAGTTGA	93710	Дb
58	·IleproAlaAs	55	Qy
93709	TGTTTGTTGGATAGCTATTCAAAGAGAATTCTTTATATTAATGTAGATACCAGCTGTGCT	93650	Db
54		54	Qy
93649	GTTTCGTGATCAGCTAGATGAAATTGAGATACTTGATTATTATTGTTTTCAGAGAAAG	93590	מט

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EU Arabidopsis sequencing, project.
Direct Submission
Submitted (18-FEB-2000) MIPS, at the Max-Planck-Institut
Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG,
lemcke@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de Proj
Coordinator: Marcel Salanoubat and Francis Quetier, Group
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Arabidopsis thaliana DNA
AL138647
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                                                                                                                                                                                                                                                                                                                              /product="receptor lectin kinase-like protein"
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/product="receptor lectin kinase-like protein"
/product="receptor lectin kinase-like protein"
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vrmptmepivpptppppkssspratkkilavolitlavastgsigolectyptprakkkyk
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shoseolymepilatistigarlehenlyrldgverhkenlylvydptprasilkyldan
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aklydgglpgtskyldpaaeistroeolygegelelllkkgllcahherilren
msavmqilngvsglpdnilldvvraenlrempersievllglnlysvgtmtlinsflsh
msavmqilngvsglpdnilldvvraenlrempersievllglnlysvgtmtlinsflsh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(2685...4127,4214...4651))
/note="strong similarity to receptor lectin kinase Arabidopsis thaliana, EMBL.U93161; Contains Protein kinases signatures and profile AA309-332; Protein ki signatures and profile AA425-437"
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DDEDGNEKKLSLISTKVMRLSIVYSHTDKQLAVTLLPAEISVPPQKSLLSLIKDLSPY
FLEETYLGFTASTGSIGALYYVMQFSYEEGVYIYPAMDLGYIPTLPPYFKKSYDRTRRI
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2685. .4
     5498. .8175
//gene="F24G16.30"
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AA339-362; Protein kinases
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                                                                                                                                                                                                                 /note="Contains ATP/GTP-binding site motif A (P-loop)
AA518-525,WW/rsp5/WWP domain signature and profile
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RRGTIPIWWGAELKMTAAEAEIYVADRDPYKGSTEYYQRLSKRYDTRNLDAPVGENQK
                                                                                                                       /product="hypothetical protein"
/protein_id="CAB75796.1"
/db_xref="GI:7019671"
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NPLTSSSSSTLRERCSPEISSLSESSASDESLAMKROGSREADGSERDPSVVCEAV
KRETGEPDGLNIADNVSGLIGKFPMVLINSIAKGCVANIAKLEIMEPCCSYKDREGSS
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TKGKVDIFVAGIGTGGTITGVGRFIKEKNPKTQVIGVEPTESDILSGGKPGPHKIQGI
GAGFIPKNLDQKINDEVIAISSEEALETHKQLALKEGLMVGISSGAAAAAAIKVAKRP
ENAGKLIAVTVNESMNAVFQVVFPSFGERYLSTPLFQSIREEVEKMQPEV
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/protein_id="CAB75795.1"
/db_xref="GI:7019670"
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KKAFYPIVCVNLLRSGEGKSECILVQHFEESMNFIKSGKLPYTRVHLINYDWHASVK LKGEQQTIEGLWNYLKSFTWAIGISEGDYLPSRQRLKDCRGEVLCIDDIEGAFCLRSH QNGVIRFNCADSLDRTNAASFFGELQYFVEQCRRLGISLDTDLGYGHNSVNNQGYNA PLPPGWEKRADAVTGKSYYIDHNYKTTTWSHPCDDKPWKRLDMRFEEFKRSTILSPVS ELADLFLQQGDIHATLYTGSKAMHSQILNIFSEESGAFKQFSAAQKNMKITLQRRYKN LLSLDENPFAPIPRRASFGATIENDPCIHAKHILVTGNTVRDKTLQSVESMSVRNWLD RAPRLNRFLIPLETERPMENDLVLELYLQPASPLAAGFRLDAFSAIKPRVTHSPSSDV VDIWPTSVIMEDRHVSPAILYIQVSVLQEQYKMVTIAEYRLPEARDGTKLYFDFPKQ complement(12393. /number=3 complement(12815. /number=2 complement(12724. complement(12490. /number=] /number-1 IQAQRVSFKLLGDVAAFTDEPAEAVDLSSRASPFAAGLSLANRIKLYYYADPYEVGKW /number=2 2.95e-114 1424.00 47.51% 41.99% 65.11% .12392) .13255) .12814) .12723) .12489)

Alignment Scores: 2.95e-114 Length: 100906
Score: 1424.00 Matches: 320
Percent Similarity: 47.51% Conservative: 42
Best Local Similarity: 41.99% Mismatches: 43
Query Match: 65.11% Indels: 360
DB: Gaps: 8

US-09-720-451-6 (1-408) x ATF24G16 (1-100906)

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3 (bases 1 to 1785)
Roje,S., Raymond,R.K., Appling,D.R. and Hanson,A.D.
Direct Submission
Submitted (01-AUG-2002) Horticultural Sciences, Uni
Florida, Hull Road, Gainesville, FL 32611, USA
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AX069359
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                 Detection of analytes using attenuat Patent: WO 0102600-A 23 11-JAN-2001; GENERAL ATOMICS (US)
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CTCACCATCAACTCACAGCCCAACATCAACGGGAAGCCGTCCTCCGACCCCATCGTGGGC
              LeuThrIleAsnSerGlnProAlaValAsnGlyGluLysSerAspSerProThrValGly
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GCCGATTTCATCATCACGCAGCTTTTCTTTGAGGCTGACACATTCTTCCGCTTTGTGAAG
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                                            TACCACTCCCTTCGGCAGCTTGTGAAGCTGTCCAAGCTGGAGGTGCCACAGGAGATCAAG
                                                                     TyrLysGlyPheIleArgMetThrGlyPheCysLysThrLysIleProAlaAspIleMet
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AR144956
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Johnson, W.G. and Stenroos, E.Scott.
Methods for diagnosing, preventing, and treating developmental
disorders due to a combination of genetic and environmental fac
patent: US 6210950-A 1 03-APR-2001;
Location/Qualifiers
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1 (bases 1 to 2187)

Johnson, W.G. and Stenroos, E.S.
Methods for diagnosing, preventing, and treating developmental disorders due to a combination of genetic and environmental factor patent; wo 0071754-A 1 30-NOV-2000;
University of Medicine and Dentistry of New Jersey (US)

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Rozen, R.
Direct S
                                                                                                                                                                                                                                           Human methylenetetrahydrofolate reductase: mapping and mutation identification Nat. Genet. 7 (2), 195-200 (1994)
                                                                                                                                                                                                                                                                                                                                artificial sequences.
1 (bases 1 to 2196)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic construct methylenetetrahydrofolate reductase (MTHFR) mRNA, complete cds.
                                                                               A candidate genetic risk factor for vascular disease: a common mutation in methylenetetrahydrofolate reductase Nat. Genet. 10 (1), 111-113 (1995)
                                                                                                                                                  2 (Dases 1 to 227)
Frosst, P., Blom, H.J., Milos, R., Goyett
R. Boers, G., den Heijer, M.,
                                                                                                                                                                                                                                                                                                Goyette, P., Sumner, J.S., Milos, R., Duncan, A.M., Matthews, R.G. and Rozen, R.
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 Submission
                                  to 2196)
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er,M., Kluijtmans,L.,
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GCATGCACCGACATGGGCATCACTTGCCCCCATCGTCCCCGGGATCTTTCCCATCCAGGGC
                                                                                                                                                         GCCGATTTCATCATCACGCAGCTTTTCTTTGAGGCTGACACATTCTTCCGCTTTGTGAAG
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McGill University - Montreal Children's
Montreal, Quebec H3H 1P3, Canada
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LERKMERKLESGDKWESLEFEPPRTAEGAVNLLSRFDRMAAGGFLY IDVTWHPAGDPG
SDKETSSMALASTAVNUGGLEFI LHUTCCRQRLEEITGHLHKAKQLGLK HIMALRGDPG
IGDQWEEEEGGFNYAVDLVKHIRSEFGDYFDICVAGYPKGHPEAGSFEADLKHLKEKV
AGADFIITQLFFEADTFFRFVKACTDMGITCPIVPGLIFPIGCHSLKHLKEKV
PQEIKDVIEP IKDNDAAIRNYGIELAVSLCQELLASGLYPGGHYSLRQLVKLSKLEV
PQEIKDVIEP IKDNDAAIRNYGIELAVSLCQELLASGLYPGGHFYTLMEARATTEVLK
RIGMWTEDDPRFULWALSAHPKRREEDVRPIFARASRPKSYIYRTQEWDEFPNGRWGNS
SSPAFGELKDYYLFYLKSKSPKEELLKWMGEELITSEASVFEVEYLYLGGEPNRRGHKV
TCLPWNDEPLAAETSLLKEELLEVNRGGILTINSQPNINGKPSSDPIVGWGPSGGYVF
OKAYLEFFTSREFAEALLQVLKXYELKWHLVNVKGENITNAFELQFNAYWGIFFG
OKAYLEFFTSREFAEALLGVLKXYELKWHLVNVKGENITNAFELQFDAAVTWGIFFG
OKAYLEFFTSREFAEALLGVLKXYELKWHLVNVKGENITNAFELQFUKDT
REIIOPTYVDFYSFMFWKDEAFALMIERWGKLYEESSPSRTIIQYIHDNYFLVNLVDN
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/protein_id="AAA74440.2"
/db_xref="GI:6139053"
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657 c 618 g
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Genet. Metabol. 64, 169-172"
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                       390 SerLeuValAspAsnAspTyr---IleAsnGlyAspLeuPheAlaValPheAlaAsp 407
                                                                                                  370 ProGluAspGluAlaSerArgLysLeuValGluGluValGlyGlySerHispheLeuVal 389
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                                                                       GAGGAGGAGTCCCCGTCCCGCACCATCATCCAGTACATCCACGACAACTACTTCCTGGTC
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                                                                                                                                                                                                                                                                                                                             AlaValAsnLysAspGlySerTrpLysSerAsnValGlyGlnThrAspValAsnAlaVal
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1, Appl	Sequence 5, Appli	7, Appl	e 8, Appl	e 2, Appl	1,	e 75, App	e 75,	75, App	e 75, App	e 75, App	e 3, Appl	e 1,	e 5, Appl	5, Appl	equence 5, Appl	e 326, Ap	4, Appl	equence 24,	e 22,	Sequence 24, Appl	22, App		13, App	11,	e 11,	e 11,	e 50,	e 7,	Ļ	7	Sequence 1, Appli	-

## ALIGNMENTS

Percent Similarity:
Best Local Similarity:
Query Match: ; DATABASE ACCESSION NUMBER: AF105977/GenBank 1-11 US-09-347-878-23 RESULT 1 US-09-347-878-23 US-09-720-451-6 (1-408) x US-09-347-878-23 (1-1971) Score: Pred. No.: Alignment Scores: APPLICAMITY YUAN, CHONG
APPLICAMITY YUAN, CHONG
APPLICATION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
FILE REFERENCE: 25885-1651
CURRENT APPLICATION NUMBER: US/09/347,878C
CURRENT FILING DATE: 1999-07-06
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 23
LENGTH: 1971
TYPE: DNA
ORGANISM: Homo sapiens Sequence 23, Application Patent No. 6376210 GENERAL INFORMATION: OTHER INFORMATION: Human OTHER INFORMATION: gene: PUBLICATION INFORMATION: FEATURE: 7.42e-110 979.00 63.72% 44.87% 44.76% US/09347878C methylenetetrahydrofolate reductase (MTHFR)
exons 1-8 Conservative: Mismatches: Indels: Length: Matches: Gaps: 1971 188 79 138 14

В

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Sequence 1, Application US/09318448
Patent No. 6210950
GENERAL INFORMATION:
APPLICANT: Johnson, William G.
APPLICANT: Stentoos, Edward S.
TITLE OF INVENTION: METHODS FOR DIAGNOSING, PR
TITLE OF INVENTION: DEVELOPMENTAL DISORDERS
FILE REFERENCE: 601-1-057
CURRENT APPLICATION NUMBER: US/09/318,448
CURRENT FILING DATE: 1999-05-25
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US-09-318-448-1
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SOFTWARE: PatentIn Ver. 2
SEQ ID NO 1
LENGTH: 2187
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ORGANISM: Homo
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                                                        GCCGTGAGCCTGTGCCAGGAGCTTCTGGCCAGTGCTTGGTGCCAGGCCTCCACTTCTAC
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                  TrpAspGlnTyrProHisGlyArgTrpGlyAspSerCysAsnProSerTyrGlyAlaLeu
                                                                                                                       GACCCC---AGGCGTCCCCTACCCTGGGCTCTCAGTGCCCACCCCAAGCGCCGAGAGGAA
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TGGGACGAGTTCCCTAACGGCCGCTGGGGCAATTCCTCTTCCCCTGCCTTTGGGGAGCTG
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TITLE OF INVENTION: CDN.
TITLE OF INVENTION: REDI
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/08738000 Patent No. 6074821
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                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC COMPUTER: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                    STREET: Continenta
CITY: Hackensack
STATE: New Jersey
                                                                                                                                                       COUNTRY: 1
ZIP: 0760
FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                         ADDRESSEE:
                                  APPLICATION NUMBER:
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US-08-738-000-3
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Query Match:
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INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: WO PO
FILING DATE: 25-MAY 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9-
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (13)...(1983)
US-09-258-928-3
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PRIOR FILING DATE: 1997-02-12
PRIOR APPLICATION NUMBER: GB 9410620.0
PRIOR FILING DATE: 1994-05-26
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 2219
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09258928 Patent No. 6218120 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 04844/005002
CURRENT APPLICATION NUMBER: US/09/258,928
CURRENT FILING DATE: 1999-03-01
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TITLE OF INVENTION: CDNA FOR HUMAN METHYLENETETRAHYDROFOLATE
TITLE OF INVENTION: REDUCTASE
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                                                                                                       GluLysLeuAspAlaLeuValAspLysCysLysAsp---ArgThrSerLeuThrTyrMet 309
                                                                                                                                                                     TrpGlyGlyProGlyGlyTyrValTyrGlnLysAlaTyrValGluPhePheCysSerLys
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                                                AlaValAsnLysAspGlySerTrpLysSerAsnValGlyGlnThrAspValAsnAlaVal
                                                                                                                                                    TGGGGCCCCAGCGGGGGCTATGTCTTCCAGAAGGCCTACTTAGAGTTTTTCACTTCCCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlyThrGluMetCysLysIleLeuAlaHisGly---IleLysThrLeuHisLeuTyr 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TACCACTCCCTTCGGCAGCTTGTGAAGCTGTCCAAGCTGGAGGTGCCACAGGAGATCAAG
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                                                                                   GAGACAGCGGAAGCACTTCTGCAAGTGCTGAAGAAGTACGAGCTCCGGGTTAATTACCAC
                                                                                                                                                                                                                      CTCACCATCAACTCACAGCCCAACATCAACGGGAAGCCGTCCTCCGACCCCATCGTGGGC
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Gaps:
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1332

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                          US-09-720-451-6 (1-408) x US-08-738-000-1 (1-2220)
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                                                                                                                                                                  Pred. No.:
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,000
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UNUMBER: WO PCT/CA95/00314
FILING DATE: 25-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMBER: GB 9410620.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08738000 Patent No. 6074821
                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: GB 9410620.0 FILING DATE: 26-MAY-1994 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 2220 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: CONTLUCTION CITY: Hackensack STATE: New Jersey COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1870 AACCTGGTGGACAATGACTTCCCACTGGACAACTGCCTCTGGCAGGTGGTGGAAGAC 1926
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CORRESPONDENCE ADDRESS:
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FEATURE:
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676 GCCGATTTCATCACGCAGCTTTTCTTTGAGGCTGACACATTCTTCCGCTTTGTGAAG 735
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                            1 AlaArgValIleValThrGlnLeuPheTyrAspThrAspIlePheLeuLysPheValAsn 20
                                                                                                                                                                                                                                                                                                                                                  nucleic acid
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                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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rpAlaSerLeuTyr 369        GGGGAAAGCTGTAT 1809	PheAsnValTrpLysAspGluAlaPheGluIleTrpSerArgGlyTr	350 1750	Qy db
CCGTCAGC 17	TGGGGCATCTTCCCTGGGCGAGAGATCATCCAGCCCACCG	9	D
9 ≥	CAATGTGAAGGGTG	1630	g B
AsnAlaVal 32	AlaValAsnLysAspGlySerTrpLysSerAsnValGlyGlnThrAspVal	310	Qy
TACGAGCTCCGGGTTAATTACCAC 1629	GAGACAGCGGAAGCACTTCTGCAAGTGCTGAAGAAGTACGAGCTCC	1570	Db
erLeuThrTyrMet 309	luLysLeuAspAlaLeuValAspLysCysLysAsp	291	Qy
CACTTCCCGC 1	TGGGGCCCCAGCGGGGGCTATGTCTTCCAGAAGGCCTACTTAGAGTTTTT	μ.	Db *
	TrpGlvGlvProGlvGlvTvrValTvrGlnLvsAlaTvrValGluP	27	٥V
 ACCCCATCGTGGGC 1509		1450	Db
erProThrValGly 270	rIleAsnSerGlnProAl	251	Qy
GGTGAACCGCCAGGGCATC 1449	CTGGCGGCTGAGACCAGCCTGCTGAAGGAGGAGCTGCTGCGGGTGA	1390	뫄
snThrLysGlyPhe 250	nProGluThrLysIleIleAsnGluGlnLeuGluLy	231	Qy
::::: ::: ACGATGAGCCC 1389	GAGAACCAAACCGGAATGGTCACAAAGTGACTTGCCTGCC	1333	Db
erGluLeuAspGly 230	lyLysLeuArgSerAsn	218	Qy
TTCTTTACCTCTCG 1332	TGGGGGGAGCTGACCAGTGAAGCAAGTGTCTTTGAAGTCTTTGTTCTTTACC	1273	Db
rgLeuTyrCysLeu 217	laValProLeuLysSerValGluAs	198	Qy
AGCTGCTGAAGATG 1272	AAGGACTACCTCTTCTACCTGAAGAGCAAGTCCCCCAAGGAGGAGCTGCT	1213	Db
161	lnPheMetArgProArgAlaA	180	Qy
CCTTTGGGGAGCTG 1212		1153	DЬ
erTyrGlyAla	pAspGlnTyrProH1sGlyArgTrpGlyAspSerCysAsnPro	160	Оу
PACCGTACCCAGGAG 1152	GATGTACGTCCCATCTTCTGGGCCTCCAGACCAAAGAGTTACATCT	1093	Db
erArgThrIleGly 159	spValArgProIlePheTrpAlaAsnArgProLysSerTyrIle	140	Qy
ACCCCAAGCGCCGAGAGGAA 1092	GACCCCAGGCGTCCCCTACCCTGGGCTCTCAGTGCCCACCCCA	1036	Дb
heArgValLysGlu 139	gSerLeuProTrpArgArgProAlaA	120	Qy
GGATGTGGACTGAG 1035	ACCCTCAACCGCGAGATGGCTACCACAGAGGTGCTGAAGCGCCTGGGGATG	976	дb
116	GluLysSerAlaLeuA	100	Qy
TTCTA	GCCGTGAGCCTGTGCCAGGAGCTTCTGGCCAGTGCCTGGTGCCAGGCCTCCAC	916	Db
Ĕ.	- 55	81	Qy
CAACTATGGCATCGAGCTG 915	GACGTGATTGAGCCAATCAAAGACAACGATGCTGCCATCCGCAACT	856	Db
yrGlyIleHisLeu 80	luGluAlaValLy	61	Qy
CACAGGAGATCAAG 855	ACCACTCCCTTCGGCAC	796	рь
- 22	rgMetThrGlyPheCysLys	41	Qy
TICCCATCCAGGGC 795	GCATGCACCGACATGGCCATCACTTGCCCCATCGTCCCCGGGGATCTTTCCCATCCA	736	DЬ
etProIleAsnAsn 40	AspCysArgGlnIleGlyIleThrCysProIleValProGlyIleM	21	Qy

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APPLICANT: COUETTE, Philippe

APPLICANT: COVETTE, Philippe

TITLE OF INVENTION: CDNA FOR HUMAN METHYLENETETRAHYDROFOLATE

TITLE OF INVENTION: REDUCTASE

FILE REFERENCE: 04644/005002

CURRENT APPLICATION NUMBER: US/09/258,928

CURRENT EILING DATE: 1999-03-01

PRIOR APPLICATION NUMBER: 08/738,000

PRIOR FILING DATE: 1997-02-12

PRIOR APPLICATION NUMBER: 08 9410620.0

PRIOR FILING DATE: 1994-05-26

NUMBER OF SEQ ID NOS: 14

SOSTMARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 2220
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Best Local Similarity:
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Pred. No.:
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US-09-258-928-1
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LOCATION: (1)
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ORGANISM: Homo sapiens
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                                                                            ThrLeuAsnMetGluLysSerAlaLeuAlaIleLeuMetAsnLeuGlyLeuIleGluGlu 119
                                                                                                                         GCCGTGAGCCTGTGCCAGGAGCTTCTGGCCAGTGGCTTGGTGCCAGGCCTCCACTTCTAC
                                                                                                                                           GlyThrGluMetCysLysIleLeuAlaHisGly---IleLysThrLeuHisLeuTyr 99
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                                                             ACCCTCAACCGCGAGATGGCTACCACAGAGGTGCTGAAGCGCCTGGGGATGTGGACTGAG
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Matches:
Conservative:
Mismatches:
Indels:
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TIT APPLANDING COLUMN C	390 1870	370 1810	350 1750	330 1690	310 1630	291 1570	271 1510	251 1450	231 1390	218 1333	198 1273	180 1213	160 1153	140 1093
T 7 -858-207A-54 uence 54, Application US/08858207A ent No. 6348328 ent No. 6348328 ent No. 6348328 ent No. 6348328 APPLICANT: Black, Michael APPLICANT: Knowles, John APPLICANT: Nicholas, Richbard APPLICANT: Stodola, Robert TITLE OF INVENTION: No. 6348328el Compounds NUMBER OF SEQUENCES: 552 CORRESPONDENCE ADDRESS: ADDRESSEE: SmithKline Beecham Corporation STREET: 709 Swedeland Road CITY: King of Prussia STATE: PA	SerLeuValAspAsnAspTyrIleAsnGlyAspLeuPheAlaValPheAlaAsp 407 :::               ::	ProGluAspGluAlaSerArgLysLeuValGluGluValGlyGlySerHisPheLeuVal 389	PheAsnValTrpLysAspGluAlaPheGluIleTrpSerArgClyTrpAlaSerLeuTyr 369 	ThrTrpGlyValPheProAlaLysGluIleIleGlnProThrIleValAspProValSer 349	AlavalAsnLysAspGlySerTrpLysSerAsnValGlyGlnThrAspValAsnAlaVal 329	GluLysLeuAspAlaLeuValAspLysCysLysAspArgThrSerLeuThrTyrMet 309	TrpGlyGlyProGlyGlyTyrValTyrGlnLysAlaTyrValGluPhePheCysSerLys 290	LeuThrIleAsnSerGlnProAlaValAsnGlyGluLysSerAspSerProThrValGly 270	LeuGlnProGluThrLysIleIleAsnGluGlnLeuGluLysIleAsnThrLysGlyPhe 250	GlyLysLeuArgSerAsn	TrpAlaValProLeuLysSerValGluAspIleTyrGluArgPheArgLeuTyrCysLeu 217	SerAspTyrGlnPheMetArgProArgAlaArgAspLysLysLeuValGluGlu 197	TrpAspClnTyrProHisGlyArgTrpGlyAspSerCysAsnProSerTyrGlyAlaLeu 179        :::::   :::	AspValArgProIlePheTrpAlaAsnArgProLysSerTyrIleSerArgThrIleGly 159

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COUNTRY: USA ZIP: 19406-0939

COMPUTER:

IBM Compatible

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FILING DATE: 14-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
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                                                                                                                                         1170
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SOFTWARE: FastSE
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                                                                                                                                                                                                                                            83 GluMetCysLysIleLeuAlaHisGlyIleLysThrLeuHisLeuTyrThrLeuAsn 102
                                                                                                                                                                                                                                                                                                                                                                                   44 PheIleArgMetThrGlyPheCysLysThr---LysIleProAlaAspIleMetAlaAla 62
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                                                                     CTAGGATA - ATAAAAGCAAACCATTCTTCTCAGGTGAGGGGAATGGTTCCTTTTAATGG
                                                                                                      LeuGlyLeuIleGlu-----GluSerLysValSerArgSerLeuPro-----Trp
                                                                                                                                       AATGCTGATACAGCAAAATACATCCATCAAGCAACCCATGCCTTGTTTAATCACCAGTCT 1229
                                                                                                                                                                                                             GACCAAATCGTGGACTTGGTAACTCAGGATGTTGCCGGTGTGCATCTCTATACGATGAAT 1169
                                                                                                                                                                                                                                                                                                           LeuGluProIleLysAspAsnGluGluAlaValLysAlaTyrGlyIleHisLeuGlyThr 82
                               ArgArgPro 131
 CAAAGACCT 1297
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FastSEQ for Windows Version
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US-08-961-527-140/c
Sequence 140, Application US/08961527
Patent No. 6420135
GENERAL INFORMATION:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                               15802 CTCGTAACTCAGCTCTTCTTTGACAATGAGCGCTTCTATGATTTTCAGGACAAGTGTATC
                              15562 GACCAAATCGTGGACTTGGTAACTCAGGATGTTGCCGGTGTGCATCTCTATACGATGAAT 15503
                                                                                                                                                          15682
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NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
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LENGTH: 28882 base pai
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SOFTWARE: ASCII Text
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CITY: Rockville
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                                                                                                                                                                                                                                                                                               GlnIleGlyIleThrCysProIleValProGlyIleMetProIleAsnAsnTyrLysGly 43
                                               GluMetCysLysIysIleLeuAlaHisGlyIleLysThrLeuHisLeuTyrThrLeuAsn 102
                                                                                                                                                        GCTCTCCGACTCTTGAAGACTTGTGAGAATATCCATCTTCCACGCAAATTTAAAGCCATC
                                                                                                                                                                                 PhelleArgMetThrGlyPheCysLysThr---LysIleProAlaAspIleMetAlaAla
                                                                                                                                                                                                                     TTGGCTGGGATTGATGTTCCCATTCATGCAGGAATTATGCCAATTCTGAATCGAAATCAG 15683
MetGluLysSerAla
                                                                                           TTAGACAAGTATGAGCATGACCCTGAGTCGCTCAGAGCAGCAGGACTTGCCTATGCAGTG
                                                                                                                      LeuGluProIleLysAspAsnGluGluAlaValLysAlaTyrGlyIleHisLeuGlyThr
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HP Vectra 486/33
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US-08-955-957A-1

Sequence 1, Applic Patent No. 6312920

Application US/08955957A

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TELEPHONE: 317-276-3334
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4848 base pairs
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                             3992 GCGCGCTTCGCCGAGCTTTCCCACGCCACCTTCCCCGAAGGTCTCGCGCGGCGGCTGGAG 4051
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HYPOTHETICAL:
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US
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MEDIUM TYPE: Floppy disk
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                          IleArgMetThrGlyPheCysLysThrLysIleProAlaAspIleMetAlaAlaLeuGlu
                                                                                                                                                      ATCACGCAGATGTTCTTCCGGGTCGAGGACTATCTGCGGGCTGCGGGACCGGGTCGCGGCC 3931
ProIleLysAspAsnGluGluAlaValLysAlaTyrGlyIleHisLeuGlyThrGluMet 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
EDNESS: single
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3932 GCCGGCTGCTGCACCCCGGTCATCCCCGGGATCATGCCCGCCACCGACGTGCGGCAGATC 3991
                                                            3872 ATCACGCAGATGTTCTTCCGGGTCGAGGACTATCTGCGGGCTGCGGGACCGGGTCGCGGCC 3931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: P-TELECOMMUNICATION INFORMATION: 317-276-3334
                                                                                                                                                                                                                                          No.:
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HYPOTHETICAL:
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ATTORNEY/AGENT INFORMATION:
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                             25 IleGlyIleThrCysProIleValProGlyIleMetProIleAsnAsnTyrLysGlyPhe 44
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                                                                                 5 ValThrGlnLeuPheTyrAspThrAspIlePheLeuLysPheValAsnAspCysArgGln
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                       LOCATION:
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Lilly Corporate Center
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                                                                                                                Query Match:
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 39,872
REFERENCE/DOCKET NUMBER: P-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3334
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APPLICANT: Rosteck Jr.,
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3872 AUCACGCAGAUGUUCUUCCGGGUCGAGGACUAUCUGCGGGCUGCGGGGACCGGGGUCGCGGCC 3931
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ANTI-SENSE:
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SYSTEM: PC-DOS/MS-DOS
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Jr., Paul R.
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                Query Match:
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                                                                                             Alignment Scores:
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GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 1556 base pairs
TYPE: nucleic acid
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NAME: White, John P.
REGISTRATION NUMBER: 28,
REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                         FEATURE:
                                                                                                                                                                                        ANTI-SENSE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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1185 Avenue of the Americas
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PARTION: NUCLEIC ACID ENCODING NEUROPEPTIDE
PRINTION: Y/PEPTIDE YY (Y2) RECEPTORS AND USES THEREOF
SQUENCES: 27
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----TACAGAAAAGCTTTCCTCTCAGCCTTCCGCTGTGAGCAGAGGTTGGATGCCATT 1257
                                                                                                                                                                                                                                                                                                                                                                                           ATTGCGATGTGCTCCACCTTCGCCAACCCCCTTCTCTATGGCTGGATGAACAGCAAC---
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                                                  TCTGGCTAGTGCATGCCACCTCCCATTGTATTGACCCTAAAAGCATCAGAGTGGAAGCCC 1479
                                                                                  AlaLysGluIleIleGlnProThrIleValAspProValSerPheAsnValTrpLysAsp
                                                                                                                     TGTGAAAGTACGTGGGTAAATTGCGACCAGAGTTGCCAACCTGGTTAGGGAAGGTTT----
                                                                                                                                                                                       GTCAAAAAGAACAATGGCCTCACTGACTCTTTTTCAGAGGCCACCAACGTGTAAGAATGC
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                                                                                                                                                                                                                                                       Best Local Similarity:
                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                          Score:
                                                                                                                                                                                                                                                                                                       Alignment Scores: Pred. No.:
                                                                                                                                                                                                                                                                                                                                                    US-09-407-367-3
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 10030
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 44'
                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 212-278-0400
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ADDRESSEE: Cooper &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1480 CAGCGGTATTGTTCCTGGAAAACTGGCTGGAAGAAT-----GAGGAGAAAATAAAC 1530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York
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                            GlyLeuIleGluGluSerLysValSerArg----
                                                                                                                           ATGGGTCCAGTTTTGTGCCATTTGGTGCCCTATGCCCAGGGTCTGGCAGTACAAGTGTCC
                                                                                          ThrLeuHisLeuTyrThrLeuAsnMetGluLysSerAlaLeuAlaIleLeuMetAsnLeu 114
                                                              ACAATAACTTTGACAGTCATTGCTTTGGACCGACATCGT - - - TGCATTGTCTACCACCTG
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Indels:
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Conservative:
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US-08-646-695-1

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CORRESPONDENCE ADDRESS:

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GENERAL INFORMATION:
APPLICANT: ROSE, John
TITLE OF INVENTION: 1
TITLE OF INVENTION: 1
NUMBER OF SEQUENCES:
                                                                                           Sequence 1, Application US/08646695 Patent No. 6168943
                                                                                                                                                                                                                                                                                                                                           1420 TCTGGCTAGTGCATGCCACCTCCCATTGTATTGACCCTAAAAGCATCAGAGTGGAAGCCC
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                                                                                                                                                                                                                                                                  CAGCGGTATTGTTCCTGGAAAACTGGCTGGAAGAAT---
                                                                                                                                                                                                                                                                                                   GluAlaPheGluIleTrpSerArgGlyTrpAlaSerLeuTyrProGluAspGluAlaSer 375
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                                                         John K.
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                                         RECOMBINANT VESICULOVIRUSES
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Best Local Similarity:
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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STATE: New Yor
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                                                                                                                                                                                                                                                                  80 LeuGlyThrGluMetCysLysLysIleLeuAlaHisGlyIleLysThrLeuHisLeuTyr
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                                         AspValArgProIlePheTrpAlaAsnArgProLysSer----
                                                                                                       GTAATCAAAATGTCTGTTACAGTCAAGAGAATCATTGACAACACAGTCATAGTTCCAAAA
                                                                                                                                                                                        ThrLeuAsnMetGluLysSerAlaLeuAlaIleLeuMetAsnLeuGlyLeuIleGluGlu
                                                                                 CTTCCTGCAAATGAGGAT---CCAGTGGAATACCCGGCAGATTACTTCAGAAAATCAAAG
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Sequence 7, Application US/08646695 Patent No. 6168943
                                                                                         GENERAL INFORMATION:
APPLICANT: ROSE, John K.
TITLE OF INVENTION: RECOMBINANT VESICULOVIRUSES
TITLE OF INVENTION: USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1525 GATGAAATGGTCCAAATGATGCTTCCAGGCCAAGAAATTGACAAGGCCGATTCATACATG
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CTCATGGATGGGCTGACAAATCAATGCAAAATGAATCAATGAACAGTTTGAACCTCTTGTG 1284
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           1155 Avenue of the Americas
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NAME: Misrock, S. Leslie
REGISTRATION UNMBER: 18,872
REFERENCE/DOCKET NUMBER: 6523
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 789-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                              186
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MEDIUM TYPE: Floppy disk
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TELEX: 66141 PENNIE
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Search completed: February 12, 2003, 17:06:31 Job time : 112 secs
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                                                                       12667 GCCTTCCACTTCTGGGGGCAA 12647
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                                                                                                                                                                         342 ProThrIleValAsp-------ProValSerPheAsnValTrpLysAspGlu 356
                                                                                                                                                                                                                                              332 -------GlyValPheProAlaLysGluIle------IleGln 341
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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Gapop 10.0 , Gapext 0.5
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   ARVIVTQLEYDTDIFLKFVN......VSLVDNDYINGDLFAVFADF 408
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US-09-258-98-4
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US-08-98-12
US-08-487-8268-12
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Qy 1 ARVIVTOLFYDTDIFLKFVNDCROIGITCDIVPGIMPINNYKGFIRMTGFCKTKIPADIM	Query Match Best Local Similarity 44.9%; Matches 188; Conservative 7	CLASSIFICATION: 514 PRIOR APPLICATION DATA: APPLICATION NUMBER: WO PCT PILING DATE: 25-MAY-1995 PRIOR APPLICATION NUMBER: BY APPLICATION NUMBER: B941 PILING DATE: 26-MAY-1994 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 656 amino acids TYPE: amino acids TYPE: amino acids TYPE: linear MOLECULE TYPE: protein US-08-738-000-4	G 6	O. 6074821 INFORMATION: OF INVENTION: OF INVENTION: FOR THE SEQUENCES: SPONDENCE ADDRES: EEFT: CONTINENTE HACKENSACK HACKENSACK TE: New Jersey	ARESULT 1 US-08-738-000-4 Sequence 4, Application US/08738000	28 85 3.9 1023 2 30 85 3.9 1023 2 31 85 3.9 2368 1 32 84.5 3.9 2368 2 33 84.5 3.9 653 2 34 83.5 3.8 616 4 35 83.5 3.8 616 4 36 83.5 3.8 653 4 37 83 82.5 3.8 1285 2 40 82.5 3.8 1285 2 41 82 3.7 291 4 42 82 3.7 291 4 44 82 3.7 918 4
QIGITCPI        DMGITCPI	Score 979; D Pred. No. 5.1 9; Mismatches	PCT/CA95/00314 5 9410620.0 4 4:	MS-DOS :e #1.0,	HUMAN	ALIGN	US-08-19 US-08-87 US-08-87 US-08-19 US-08-19 US-08-71 US-09-13 US-09-43 US-09-43 US-08-67 US-08-67 US-08-67 US-08-67 US-08-67 US-08-67 US-08-67 US-08-67 US-08-67 US-08-67 US-08-67 US-08-67 US-08-67 US-08-67
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CURRENT APPLICATION NUMBER: US/09/258,928
CURRENT FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: 08/738,000
PRIOR FILING DATE: 1997-02-12
PRIOR APPLICATION NUMBER: GB 9410620.0
PRIOR FILING DATE: 1994-05-26
VUMBER OF SED ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 656
TYPE: PRT
ORGANISM: Homo sapiens
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Best Local
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APPLICANT: ROYETTE, Philippe
APPLICANT: GOYETTE, Philippe
TITLE OF INVENTION: CDNA FOR HUMAN METHYLENETETRAHYDROFOLATE
TITLE OF INVENTION: REDUCTASE
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ETAEALLQVLKKYELRVNYHLVNVKGENITNAPELQPNAVTWGIFPGREIIQPTVVDPVS
                     LQPETKIINEQLEKINTKGFLTINSQPAVNGEKSDSPTVGWGGPGGYVYQKAYVEFFCSK
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                                                                                                                                                                               SDYQ--FMRPRARDKKLVEEWAVPLKSVEDIYERFRLYCLGKLRSN-----PWSELDG
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                                                                                                                                                                                                                                                      SKYSRSLPWRRPANYFRYKEDYRPIFWANRPKSYISRTIGWDQYPHGRWGDSCNPSYGAL 179
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                                                                       LAAETSLLKEELLRVNRQGILTINSQPNINGKPSSDPIVGWGPSGGYVFQKAYLEFFTSR
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44.9%; Pred. No. 5.1e-91;
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US-09-347-878-24
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US-08-738-000-2
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CURRENT FILING DATE: 1999-07-06
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 24
LENGTH: 656
                                                             Sequence 2, Application US/08738000
Patent NO. 6074821
GENERAL INFORMATION:
TITLE OF INVENTION: CDNA FOR HUI
TITLE OF INVENTION: REDUCTASE
NUMBER OF SEQUENCES: 14
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: METHODS AND COMPOSITIONS FILE REFERENCE: 25885-1651
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TYPE: PRT
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                                                CORRESPONDENCE ADDRESS:
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REDUCTASE
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Pred. No. 5.1e-91
9; Mismatches 13
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                 Hackensack
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GENERAL INFORMATION:
APPLICANT: ROZEN, Rima
APPLICANT: ROZEN, Philippe
APPLICANT: GOYETTE, Philippe
APPLICANT: GOYETTE, Philippe
TITLE OF INVENTION: CDNA FOR HUMAN METHYLENETETRAHYDROFOLATE
TITLE OF INVENTION: REDUCTASE
FILE REFERENCE: 04844/005002
CURRENT APPLICATION NUMBER: US/09/258,928
CURRENT FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: 08/738,000
PRIOR FILING DATE: 1997-02-12
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Best Local Similarity
Matches 188; Conserv
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 660 amino acida
                                                                                                                                                                                                                Sequence 2, Application US/09258928 Patent No. 6218120
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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44.9%; Pred. No. 5.1e-91;
tive 79; Mismatches 138; Indels 14;
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US-08-858-207A-324
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PRIOR FILING DATE: 1994-05-26
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA: APPLICATION MARBER: US/08/858,207A FILING DATE: 09-MAY-1997
                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                     APPLICANT: Knowles, David
APPLICANT: Nicholas, Richard
APPLICANT: Stodola, Robert
TITLE OF INVENTION: No. 6348328el Compounds
NUMBER OF SEQUENCES: 552
                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Black, Michael APPLICANT: Hodgson, John
                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            584 FMFWKDEAFALWIERWGKLYEEESPSRTIIQYIHDNYFLVNLVDNDFPLDNCLWQVVED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             286 DVIEPIKDNDAAIRNYGIELAVSLCQELLASGLVPGLHFYTLNREMATTEVLKRLGMWTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     226 ADFIITQLFFEADTFFRFVKACTDMGITCPIVPGIFPIQGYHSLRQLVKLSKLEVPQEIK 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 AALEPIKDNEEAVKAYGIHLGTEMCKKILAHG-IKTLHLYTLNMEKSALAILMNLGLIEE 119
                                                                                                                                                                                                   STREET: 709 Swederand CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ARVIVTQLEYDTDIFLKFVNDCRQIGITCPIVPGIMPINNYKGFIRMTGFCKTKIPADIM 60
                                                                                           COMPUTER: IBM Compatible
                                                                                                                                                                       COUNTRY:
                                                                           OPERATING SYSTEM:
                                                                                                                                                     ZIP: 19406-0939
                                                                                                                                                                                                                                 ADDRESSEE: SmithKline STREET: 709 Swedeland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LQPETKIINEQLEKINTKGFLTINSQPAVNGEKSDSPTVGWGGPGGYVYQKAYVEFFCSK 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FNVWKDEAFEIWSRGWASLYPEDEASRKLVEEVGGSHFLVSLVDNDY-INGDLFAVFAD 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ETAEALLQVLKKYELRVNYHLVNVKGENITNAPELQPNAVTWGIFPGREIIQPTVVDPVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAAETSLLKEELLRVNRQGILTINSQPNINGKPSSDPIVGWGPSGGYVFQKAYLEFFTSR 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KDYYLFYLKSKSPKEELLKMWGEELTSEASVFEVFVLYLSGEPNRNGHKVTCLPWND-EP
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                                                                                                                                                                                           PA
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Knowles, David
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                                                                                                                                                                           USA
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44.9%; Pred. No. 5.1e-91;
tive 79; Mismatches 138; Indels 14;
                                                                             DOS
                                                                                                                                                                                                                                   Road
                                                                                                                                                                                                                                                     Beecham Corporation
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PRIOR APPLICATION DATA:

APPLICATION NUMBER:

60/017670

CLASSIFICATION:

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US-08-955-957A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear
; MOLECULE TYPE: No. 6348328e
US-08-858-207A-324
       Matches
                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/08955957A Patent No. 6312920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                          REFERENCE/DOCKET NUMBER: P-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3334
                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: SAM OPERON NUMBER OF SEQUENCES: 6
                                                                            MOLECULE TYPE:
                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 305 amino acid
                                                                                                                                                                                                                                APPLICATION NUMBER: US/0
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                           TOPOLOGY:
                                                                                                        TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        227
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                   Local Similarity
                                                                                                                                                                                                        NAME: Webster, Thoma REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                           STREET: Lilly Corpo
CITY: Indianapolis
STATE: Indiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 LEPIKDNEEAVKAYGIHLGTEMCKKILAHGIKTLHLYTLNMEKSA 107
                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Gimmi, Edward REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 IVTQLFYDTDIFLKFVNDCRQIGITCPIVPGIMPINNYKGFIRMTGFCKT-KIPADIMAA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX:
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        30;
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                                                                                                       amino acid
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                                                                                                                 305 amino acids
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Lilly Corporate Center
     Conservative
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                                                                                        linear
                                                                          protein
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                                                                                                                                                                                                                    Thomas
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                6.3%;
                                                                                                                                                                                                                                                                             US/08/955,957A
                                                                                                                                                                                                       39,872
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     18;
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Score 138; DB 4; Pred. No. 8.6e-06; 13 matches 62;
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                                                                                                                                                                                           P-10162
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Pred. No. 6.7e-07;
2; Mismatches 49
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                                                                                                                                                                                                                                                                                                       #1.30
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                             Length 305;
  Indels
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Gaps
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Best Local Similarity
"atches 88; Conserve
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TELEPAX: (619) 43-11.

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:

TENGTH: 2710 amino acids
                                                                                                                                                                                                                                                                     MOLECULE TYPE: I
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Plas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, xin-zhaun
APPLICANT: Wellems, Thomas E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: NI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                      171 S---
                                                227 --FGKIYEKLNGAEARYGNDPEFFKLRED----WWTANR-----ETV-WKAITCNAWGN 273
                                                                               112 MNLGLIEESKVSRSLPWRRPANVFRVKEDVRPIFW-ANRPKSYISRTIGWDQYPHGRWGD 170
                                                                                                                 182 PSQICTMLARSFADIGDIVRGRDLYLGNPQEIKQRQQLENNLKTI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                              56 PADIMAAL-EPIKDNEEAVKAYGIHLGTEM----CKKILAHGIKTLHLYTLNMEKSALAIL 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     239 AARGNPAEGHRIGVEYATAMAGRLLAEGAPGLHYITLNRSTATLEIHRNI 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179 ITOMFFRVEDYLRLRDRVAAAGCCTPVIPGIMPATDVRQIARFAELSHATFPEGLARRLE 238
                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/0 FILING DATE: 07-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 PIKDNEEAVKAYGIHLGTEMCKKILAHGIKTLHLYTLNMEKSALAILMNL 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSEE: Knobbe Martens Olson & Bear T: 620 Newport Center Drive 16th Newport Beach
                                                                                                                                                                                                                                                                                                                                                                 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/08568459A
                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                    Plasmodium falciparum
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Wellems, Thomas E.
                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                    protein
NO
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                                                                                                                                                                                                                                                                                                                                                 single
                                                                                                                                                                            4.5%; pre
19.8%; pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BINDING DOMAINS FROM PLASMODIUM VIVAX AND PLASMODIUM FALCIPARUM ERYTHROCYTE 37
-CN----PSYGALSDY--QFMRPRARDKKLVEEWAVPL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/08/568,459A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29,655
                                                                                                                                                                                   Score 97.5; DB Pred. No. 3.6; 59; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH121.001CP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16th Floor
                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                    142;
                                                                                                                                                                                                                  Length 2710;
                                                                                                                                                                                 Indels 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BINDING PROTEINS
                                                                                                                   ---- 226
                                                                                                                                                                               Gaps
                  202
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Indels

155;

Gaps

27;

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US-08-487-826B-12
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                                       US-08-487-826B-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12, Appr-
Sequence 12, Appr-
Sequence 12, Appr-
Query Match
                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
APPLICATION NUMBER: US/08/
EILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: TETABLED NAGION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                               TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 92660

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIFARUM ERYTHROCYTE BINDING PROTEINS
                                                                                            MOLECULE TYPE: pr
                                                                                                                                                                                                                                                                                      NAME: ISTAELSEN, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
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                                                                             ORIGINAL SOURCE
                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 2710 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                   STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                     TELEPHONE:
                                                            ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FYDELNKSEYRTVDKFLEKLSNEEICTKVKDEEGGTIDFKNVNSD----STSGASGTNVE 487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KKIKDVKRNCRGKDKEDKDRYCSRNGYDCEKTKRAIGKLRYGKQCISCLYACNPYVDWIN
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                                                                                                                                                                       amino acid
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Chitnis, Chetan
Miller, Louis H.
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Wellems, Thomas E.
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                                                          Plasmodium falciparum
                                                                                                                                                                                                                                                                     (619) 235-8550
                                                                                                              protein
4.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Release #1.0,
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                                                                                                                                                                                                                                                                                                             NIH121.001CP1
Score 97.5;
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16th
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Length 2710;
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US-09-210-288-12
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                                                                                                                                                  ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,288
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                  REGISTRATION NUMBER: 36,516
REFERENCE/DOCKET NUMBER: NIH121.1FWDV1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Fuller, Michael
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               330 TWGVFPAKEIIQP-----TIVDPVSFNVWKDEAFEIWSRGWASLY---PEDEASRKLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 PSQICTMLARSFADIGDIVRGRDLYLGNPQEIKQRQQLENNLKTI----------- 226
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                                                                                                                                                                                                                                                                                                                                                 STREET: 620 Newport Center Drive CITY: Newport Beach STATE: California
                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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Chitnis, Chetan
Chitnis, Louis H.
Miller, Louis H.
Peterson, David S.
(619) 235-0176
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9; Mismatches
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US-09-210-288-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 4.5%; Score 97.5; Best Local Similarity 19.8%; Pred. No. 3 Matches 88; Conservative 59; Mismatche
                                                                                                                                                                                                                                                                                                                                Sequence 14,
                                                                                                                                                                                                                                                                                                                                                -08-487-826B-14
                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Sim, K
APPLICANT: Chitni
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SEQUENCE CHARACTERISTICS:
LENGTH: 2710 amino acids
                                                                                                                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                      APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING
NUMBER OF SEQUENCES: 45
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                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                         CORRESPONDENCE ADDRESS
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STRANDEDNESS: si
TOPOLOGY: linear
                                                             COUNTRY:
                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56 PADIMAAL-EPIKDNEEAVKAYGIHLGTEM----CKKILAHGIKTLHLYTLNMEKSALAIL 111
   COMPUTER:
                                                                                                            STREET:
                                                                                                                             ADDRESSEE:
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T: 620 Newport Center Drive 16th Floor
Newport Beach
                                                  92660
                                                                                                                                                                                                                                                                                                                4, Application US/08487826B
5993827
                                                                              California
                                                                                                                                                                                                                                                  Chitnis, Chetan
Miller, Louis H.
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E: Floppy disk
IBM PC compatible
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                                                                                                                                                                                                                                     David S.
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US-08-646-695-2

US-08-08-646-695-2

; Sequence 2, Application US/08646695

; Patent No. 6168943

; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 4.5%; Score 97.5; Di
Best Local Similarity 19.8%; Pred. No. 4.3;
Matches 88; Conservative 59; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (619) 235-0176 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: NI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                       APPLICANT: Rose, John K.
TITLE OF INVENTION: RECOMBINANT VESICULOVIRUSES AND THEIR
TITLE OF INVENTION: USES
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 3060 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                               544 LKSGKGHDDIEEKLNKFCDEKNGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 380 EEVGGSHFLVSLVDN----DYINGD 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            330 TWGVFPAKEIIQP-----TIVDPVSFNVWKDEAFEIWSRGWASLY---PEDEASRKLV 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    430 FYDELNKSEYRTVDKFLEKLSNEEICTKVKDEEGGTIDFKNVNSD----STSGASGTNVE 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              226 SELDGLQPETKIINEQLEKINTKGFLTINSQPAVNGEKSD---SPTVGWGGPGGYVYQKA 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         322 KKIKDVKRNCRGKDKEDKDRYCSRNGYDCEKTKRAIGKLRYGKQCISCLYACNPYVDWIN 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        225 --FGKIYEKLNGAEARYGNDPEFFKLRED----WWTANR-----ETV-WKAITCNAWGN 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112 MNLGLIEESKVSRSLPWRRPANVFRVKEDVRPIFW-ANRPKSYISRTIGWDQYPHGRWGD 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 PSQICTMLARSFADIGDIVRGRDLYLGNPQEIKQRQQLENNLKTI------ 224
ADDRESSEE: PENNIE & ELMVILL STREET: 1155 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/0 FILING DATE: 10-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 PADIMAAL-EPIKDNEEAVKAYGIHLGTEM---CKKILAHGIKTLHLYTLNMEKSALAIL 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S-----CN----PSYGALSDY--QFMRPRARDKKLVEEWAVPL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NQKEQFDKQKKKYDEEIKKYE----NGASGGSRQKRDAGGTTTTNYDG-----YEKK 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYFHATCNRGERTKGYCRCNDDQVPTY---FDYVPQYLR-----WFEEWAEDFCRKKN 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Y------VEFFCSKEKLDALVDKCKDRT--SLTYMAVNKDGSWKSNVGQTDVNAV 329
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linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
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                                                                                                                                                                                                                                                                                 RESULT 13
                                                                                                                                                                                                         Sequence 2, Application PC/TUS9606053
GENERAL INFORMATION:
APPLICANT: Yale University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 4.4%;
Best Local Similarity 19.7%;
Matches 63; Conservative 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                          TITLE OF INVENTION:
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9TP: 10036-2711
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 DASRTSADDKWLPLYLLGLYRVGRTQMPEYRKKLMDGLTNQCKMINEQFEPLVPEG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                         306 LTYMAVNKDGSWKSNVGQTDVNAVTW------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/646,695
FILING DATE: On Even Date Herewit
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE:
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                                    COUNTRY: USA
ZIP: 10036-2711
                                                                       STATE:
                                                                                      CITY: New York
                                                                                                      STREET:
                                                                                                      ADDRESSEE: PENNIE & EDMONDS STREET: 1155 Avenue of the
                                                                                                                                                                                                                                                                                                                                                                     ---PVSFNVWKDEAFEIWSR 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------RFRLYCLGKLRSNPWSE--LDGLQPETKIINEQLEKINTKGFLTI 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PVEYPADYFRKSKEI-PLY-INTTKSLSDLRGYVYQGL------KSGNVSIIHVN 70
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                                                                     New York
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                                                                                                                                                                                         Yale University
VENTION: RECOMBINANT VESICULOVIRUSES AND THEIR
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Floppy disk
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Pred. No. 0.
                                                                                                        Americas
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                                                                                                                                                                                                                                                                                                                                    RESULT 14
US-08-965-762-23
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                                                     ; ORGANISM: Saccharomyces cerevisiae US-08-965-762-23
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                                                                                  APPLICANT: Koltin, Yigal
APPLICANT: Gavrias, Victoria
APPLICANT: Gavrias, Victoria
TITLE OF INVENTION: ESSENTIAL FUNGAL GENES AND THEIR USE
FILE REFERENCE: 07334/062001
CURRENT FILING DATE: 1997-11-07
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FRASTSEQ for Windows Version 3.0
SEQ ID NO 23
LENGTH: 347
TYPE: PRT
                                                                                                                                                                                                                                                                            Sequence 23, Application US/08965762
Patent No. 6280963
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 19.7 Matches 63; Conservative
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                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (212) 869-97
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC:
FILING DATE: 01-MAY-199
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LENGTH: 422 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 65:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127 PWRRPANVFRVKEDVRPIFWANRPKS-----YISRTIGWDQYPHGRWGDSCNPS----- 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123
                                                                                                                                                                                                                                                                                                                                                                                                                                             347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 --- YGALSDYQFMRPRARDKKLVEEWA------
                                                                                                                                                                                                                                                                                                                                                                                                          283 LSSKSPYSSVKNPAFHFWGQ 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 SYLYGALKDIR------GKLDKDWSSFGINIGKAGDTIGIFDLVSLKALDGVLPDGVS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                           ---PVSFNVWKDEAFEIWSR 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LTYMAVNKDGSWKSNVGQTDVNAVTW-------GVFPAKEI-----IQPTIVD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NSQPAVNGEKSDSPTVGWGGPGGYVYQKAYVEFF-----CSKEKLDALVDKCKDRTS 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DASRTSADDKWLPLYLLGLYRVGRTQMPEYRKKLMDGLTNQCKMINEQFEPLVPEG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------RDIFDV-WGNDSNYTKIVAAVDMFFHMFKKHECASFRYGTIVSRFKDCAA 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------RFRLYCLGKLRSNPWSE--LDGLQPETKIINEQLEKINTKGFLTI 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LATE-----GHLCKITGMSTEDVTTWILNREVADEMVQMMLPGQEIDKADSYMPYLIDFG 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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 4.2%;
21.3%;
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   Score
Pred.
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   91;
No.
   DB 4;
0.65;
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                  Length 347;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 124;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178
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CURRENT APPLICATION NUMBER: US/09/911,927
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 08/965,762
PRIOR FILING DATE: 1997-11-07
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 23
LENGTH: 347
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-09-911-927-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
US-09-911-927-23
; Sequence 23, Applic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: KOLTIN, Yigal
APPLICANT: Gavrias, Victoria
TITLE OF INVENTION: ESSENTIAL FUNGAL GENES AND THEIR USE
FILE REFERENCE: 06286-062003
                                                                                                                                                                                                                                                                                                                                            Query Match 4.2%; Score 91; Best Local Similarity 21.3%; Pred. No. Matches 78; Conservative 57; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
       209
                                                                                                             110 GIDWIGAVKEVFTNPLEAVTNPTYKIQLVGVKSKDDMGLIFQANVFGPYYFISKIL--PQ 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       333 DEKLKDQ 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     297 VDKCKDR 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           286 NPNFEKQDVKYGSATSRDGMPYIKTQEID------PTGMSDVFAYIQ----KKKLE-W 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168 LTRGKAYIVWISSIMSDPKYLSLNDIELLKTNASYEGSKRLVD--LLHLATYKDLKKLGI 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163 YPHGR----WGDS--CNPSYGALSDYQFMRPRAR---DKKLVEEWAVPLKSVEDI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114 ----LGLIEESKVSRSLPWRRPANVFRV-----KEDVRPIFWAN--RPKSYISRTIGWDQ 162
                                                                                                                                                                                         72 LLVDFTNMVSVLNAY------109
                                                                                                                                                                                                                           62 ALEPIKDNEEAVKAYGIHLGTEMCKKILAHGIKTLHLYTLNMEKSALAIL-MN------ 113
                                                                                                                                                                                                                                                                   22 RLIETE---DINVRLTIVVTSR----TLPRVQEV--INQIKDFYNKSGRVE-DLEIDFDY 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72
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                                                                                                                                                                                                                                                                                                       2 RVIVTQLFYDTDIFLKFVNDCRQIGITCPIVPGIMPINNYKGFIRMTGFCKTKIPADIMA 61
                                   LTRGKAYIVWISSIMSDPKYLSLNDIELLKTNASYEGSKRLVD--LLHLATYKDLKKLGI 225
                                                                     YPHGR----WGDS--CNPSYGALSDYQFMRPRAR---DKKLVEEWAVPLKSVEDI-----
                                                                                                                                                   ----LGLIEESKVSRSLPWRRPANVFRV-----KEDVRPIFWAN--RPKSYISRTIGWDQ 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEQLEKINTK-GFLTI-NSQPAVNGEKSDSPTVGWGGPGGYVYQKAYVEFFCSKEKLDAL 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NQYVVQPGIFTSHSFSEYLNFFTYFGMLCLFYLARLLGSPWHNIDGYKAANAPVYVTRLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----YERFRLYC---IGKLRSNPWSELDGLQPE-----TKII 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GIDWIGAVKEVFTNPLEAVTNPTYKIQLVGVKSKDDMGLIFQANVFGPYYFISKIL--PQ 167
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-YERFRLYC---LGKLRSNPWSELDGLQPE-----TKII 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57;
                                                                                                                                                                                                                                                                                                                                                Mismatches 118;
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                                                                                                                                                                                                                                                                                                                                                                  0.65;
                                                                                                                                                                                                                                                                                                                                                                                  DB_4; Length 347;
                                                                                                                                                                                                                                                                                                                                            Indels 114; Gaps
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Search completed: February 12, 2003, 17:04:04 Job time: 38 secs

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Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                            Database :
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                                                                                                                                                  spTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_manmal:*
7: sp_mbc:*
8: sp_organelle:*
9: sp_phage:*
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Gapop 10.0 , Gapext 0.5
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2187
1 ARVIVTQLFYDTDIFLKEVN.....VSLVDNDYINGDLFAVFADF 408
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Copyright (c) 1993 - 2003 Compugen Ltd.
Sp_plant: *
sp_rodent: *
sp_vartebrate: *
sp_vertebrate: *
sp_unclassified: *
sp_rvirus: *
sp_rvirus: *
sp_bacteriap: *
sp_archeap: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

16	15	14	13	12	11	10	9	8	7	6	ъ	4	ω	2	1	Result
188	189	189	193	196	197.5	198	215	221	222	246	1762	1777	1831	1834	1834	Score
8.6	8.6	8.6	8.8	9.0	9.0	9.1	9.8	10.1	10.2	11.2	80.6	81.3	83.7	83.9	83.9	Query Match
282	296	296	307	295	163	313	275	314	290	276	593	592	594	594	594	Length DB
16	16	16	16	16	ω	16	16	16	16	16	10	10	10	10	10	BB
Q9PN93	Q8X766	Q8Z302	Q9S2V3	Q9CP31	094090	Q92NK1	Q9PEA7	Q9A6F4	Q91687	Q8Y389	Q9SE94	Q9SE60	Q9SUJ0	Q94JZ1	Q9SE59	ID
Q9pn93 campylobact	Q8x766 escherichia	Q8z302 salmonella	Q9s2v3 streptomyce	Q9cp31 pasteurella	094090 saccharomyc	Q92nk1 rhizobium m	7	Q9a6f4 caulobacter	Q9i687 pseudomonas	Q8y389 ralstonia s	Q9se94 zea mays (m	Q9se60 arabidopsis	_	Q94jz1 arabidopsis	Q9se59 arabidopsis	Description

444	40 42 42	3333 367 6	3 4 0	2 2 2 2 2 2 2 3 2 4	28 29 30	25 26 27	223	17 18 19 20
99.5 99 98.5	100 100	102	104.5	142 138	155.5 154.5 148.5	163 162.5 162	179 179 171	186 184 182 182
444	444	44.7			7.1 7.1 6.8	7.5 7.4	7.8	
619 406 582	548 422 1142	920 301	1138	318 305	349 130 288	283 305 274	312 304	293 183 292 292
5 12 16	3 16	13 5 1	12	122	16	16 16	16 16	216
Q9VMI9 Q83136 Q67141	Q9P8J5 Q88993 Q97J24	Q9/10A4 Q9/10A4 Q9/10A4 Q8/10A4	Q9PKQ7	Q9F3S4 Q938W5	Q9VTI0 Q9ACM5 Q97S30	Q9CG56 Q98K87 Q8Y186	Q8ZJI6 Q8UDK2 Q9KNP6	Q9L5C1 Q9N0Y5 Q9JZQ3 Q9JUT7 Q9JUT7
Q9vmi9 drosophila Q83136 bean yellow 067141 aquifex aeo	Q9p8j5 candida alb Q88993 vesicular s Q97j24 clostridium		Q9pkq7 chlamydia m Q9qd13 clover yell	Q9f3s4 rhodothermu Q938w5 streptomyce O8til7 methanosarc	Q9vtiO drosophila Q9acm5 streptococc Q97s3O streptococc	Q9cg56 lactococcus Q98k87 rhizobium l Q8yi86 brucella me	$\omega N \omega$	Q915c1 leptospira Q9n0y5 sus scrofa Q91zq3 neisseria m Q9jut7 neisseria m Q9jut8 photorhabdu

## ALIGNMENTS

DR DR	DR R	R P	R S	5 Z	R A	R.A	RA	RA	RA	2 7	2 2	P.	22.7	RT	RT	RA	R.A	RX	RP	RN	o <b>x</b>	8	ದ್ದ	8	SO	Œ	DE	DI.	3 5	A C	B	298	RESULT
HSSP; P00394; 1B5T. InterPro; IPR000194; ATPase_a/bcentre.	EMBL; Ar050434; AAK91450.1;	ted (AUG-2001) to the	icorogra ii., wonce		eki M.,	Palm C.J.,	B., Lee J.M., Lin	., Kamiya A.,	Dale J.M., Goldsmith A.D.	Chart Chart D win C T Wassens F		J. Biol. Chem. 274:36089-36096(1999).	higher plants.";	encoding NADH-dependent methylenetetrahydrofolate reductase from	"Isolation, characterization and functional expression of cDNAs	Bohnert H.J., Hanson A.D.;			SEQUENCE FROM N.A.	[1]		eurosids II; Brassicales; Brassicaceae; Arabidopsis.	edons; core eu	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Arabidopsis thaliana (Mouse-ear cress).		trahydrofola	(TrEMBLrel. 21,	01-MAY-2000 (TREMBLIGH: 13) CLEAST SEQUENCE UDDATE)	ن	Q9SE59 PRELIMINARY; PRT; 594 AA.		DUT 1

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                                     A Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
A Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
AR Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawi J.,
AR Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
AR Sakurai T., Satou M., Seki M., Sinn P., Yamada K., Shinozaki K.,
AR Sakurai T., Theologis A., Davis R. W.;
AR Ecker J., Theologis A., Davis R. W.;
AR Ecker J., Theologis A., Davis R. W.;
BR ECKER J., Theologis A., Davis R. W.;
AR Interpro; IPR000194; ATPASE_A/Dentre.
BR Interpro; IPR000194; ATPASE_A/Decntre.
BR Interpro; IPR000194; ATPASE_A/Decntre.
BR Interpro; IPR0003171; Mehydrof_redctse.
BR Interpro; IPR0003171; Mehydrof_redctse.
BR Ffam; PF02219; MTHFR; 1.
BR TIGREMAN; TIGR00677; fadh2_euk, 1.
BR PROSITE; PS00152; ATPASE_A/LPHA_BETA; UNKNOWN_1.
SQ SEQUENCE 594 AA; 66842 MW; 14D664CFDE7CD8DE CRC64;
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          Query Match
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Best Local
                                                                                                                                                                                                                                                                                                           Q94JZ1 PRELIMINARY; PRT; 594 AA.
Q94JZ1;
Q94JZ1;
Q1-DEC-2001 (Trembirel. 19, Created)
Q1-DEC-2001 (Trembirel. 19, Last sequence update)
Q1-DEC-2001 (Trembirel. 21, Last sequence update)
Q1-JUN-2002 (Trembirel. 21, Last annotation update)
Putative methylenetetrahydrofolate reductase.
Arabidopsis thaliana (Mouse-ear cress).
Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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InterPro; IPR003171; Mehydrof_redctse.
Pfam: PF0219; MrHER; 1.
TIGREAMS; TIGR00677; fadh2_euk; 1.
PROSITE; PS00152; ATPASE_ALPHA_BETA; UNKNOWN_1.
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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Pred. No. 1.6e
37; Mismatches
                  Score 1834;
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..6e-148;
hes 36;
                 DB 10;
                 Length 594;
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Matches
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InterPro; IPRO04621; FadhZ_euk.
InterPro; IPRO034621; FadhZ_euk.
InterPro; IPR003471; Mehydrof_redctse.
Pfam; PF02219; MTHFR; 1.
TIGRRAMS; TIGR06677; fadhZ_euk; 1.
PROSITE; PS00152; ATPASE_ALPHA_BETA; UNKNOWN_1.
Oxidoreductase.
SEQUENCE 594 AA; 66803 MW; 64859A988DA81657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Ravanel 5., Rebeille F., Douce R.;
"FOLAte metabolism in higher plants: cloning of methylenetetrahydrofolate reductase in Arabido Submitted (JUL-1999) to the EMBL/GenBank/DDBJ EMBL, AJJ45414; CAB53783.1; -...
HSSP; P00394; 185T.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop
Spermatophyta; Magnoliophyta; eudicottyledons; core eudicots;

Brassicales; Brassicaceae; Arabidopsis.
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Q1-MAY-2000 (TrEMBLrel. 13, Created)

Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)

Q1-UN-2002 (TrEMBLrel. 21, Last annotation update)

Methylenetetrahydrofolate reductase (EC 1.5.1.20).
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AALEPIKDNEEAVKAYGIHLGTEMCKKILAHGIKTLHLYTLNMEKSALAILMNLGLIEES
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34; Conservative
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01-MAY 2000 (TREMBLIE1. 13, Created)
01-MAY 2000 (TREMBLIE1. 13, Last sequence update)
01-JUN-2002 (TREMBLIE1. 11, Last sequence update)
01-JUN-2002 (TREMBLIE1. 21, Last annotation update)
Methylenetetrahydrofolate reductase MTHFR1 (EC 1.5.1.20) (Putative methylenetetrahydrofolate reductase MTHFR1).
E24G16. 240 OR AT3559970.
E24G16. 240 OR AT3559970.
E24G16. 240 OR AT3559970.
E24G16. 240 OR AT3559970.
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E24G16. 240 OR AT3570.
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Yamada K., Banh J., Chang C.H., Chang E., Dale J.M., Goldsmith A.D., Yamada K., Banh J., Chang C.H., Tang C., Toriumi M., Wu H.C., Lee J.M., Ondera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R. Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J., Meyers M.C., Miranda M., Seki M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
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Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
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J. Biol. Chem. 274:36089-36096/1999\
                                    Shinn P., Southwick A., Shinozaki K., Davis R. Theologis A.;
"Full Length cDNA of gene At3g59970 (GI:152322 Submitted (DEC-2001) to the EMBL/GenBank/DDBJ EMBL, AF181966; AAD55787.1; -. EMBL; AF181967; CAB75816.1; -. EMBL; AY070034; AAL49791.1; -. EMBL; P00394; 1857.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
         A,
         66429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81.3%;
         MW;
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4568996775B638B4 CRC64;

expression of reductase

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InterPro; IPR004621; Fadh2_euk.
InterPro; IPR003171; Mehydrof_redctse.
Pfam; PF02219; MTHER; 1.
TIGRFAMS; TIGR00677; Fadh2_euk; 1.
PROSITE; PS00152; ATPASE_ALPHA_BETA; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oxidoreductase.
SEQUENCE 592 AA; 66288 MW; 72D7453AF1AF1573 CRC64;
Spermatophyta; Magnoliophyta; Li
Panicoideae; Andropogoneae; Zea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WSRSWANLYPEDDPSRKLLEEVKNSYYLVSLVDNNYINGDIFSVFA
                                                                                                                                                                                                                                                                                                                                                                                                                               QLEKINTKGFLTINSQPAVNGEKSDSPTVGWGGPGGYVYQKAYVEFFCSKEKLDALVDKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KVSRSLPWRRPANVFRVKEDVRPIFWANRPKSYISRTIGWDQYPHGRWGDSCNPSYGALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AALEPIKDNEEAVKAYGIHLGTEMCKKILAHGIKTLHLYTLNMEKSALAILMNLGLIEES
                                                                                                                                                                                                                                                                                                                                                     KDRTSLTYMAVNKDGSWKSNVGQTDVNAVTWGVFPAKEIIQPTIVDPVSFNVWKDEAFEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KISRSLPWRRPANVFRTKEDVRPIFWANRPKSYISRTKGWNDFPHGRWGDSHSAAYSTLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AALEPIKDNDEAVKAYGIHFATEMCKKILAHGITSLHLYTLNVDKSAIGILMNLGLIDES
                                                                                                                                                                                                                                                                                             WSRGWASLYPEDEASRKLVEEVGGSHFLVSLVDNDYINGDLFAVFA 406
                                                                                                                                                                                                                                                                                                                                KAFPSITYMAVNKSENWVSNTGESDVNAVTWGVFPAKEVIQPTIVDPASFKVWKDEAFEI
                                                                                                                                                                                                                                                                                                                                                                                                        QLGKINSNGFLTINSQPSVNAAKSDSPAIGWGGPGGYVYQKAYLEFFCSKDKLDTLVEKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cred. No. 1.2e-143;
44; Mismatches 43.
              Streptophyta; Embryophyta; Tracheophyta; yta; Liliopsida; Poales; Poaceae; PACC clade;
                                                                   3, Last sequence update)
1, Last annotation update)
reductase (EC 1.5.1.20).
                                                                                                                             Created)
                                                                                                                                                                    593
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187 61

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Query Match
Best Local S
Matches 47
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XX MEDILNE-21681879; PubMed-11823852;
XX MEDILNE-21681879; PubMed-11823852;
XX MEDILNE-21681879; PubMed-11823852;
XX MEDILNE-21681879; PubMed-11823852;
XX MEDILNE-21681879; PubMed-11823852;
XX MEDILNE-21681879; Canual J. Canual J. Cattolico L.,
XX Arlat M., Billault A., Brottier P., Canual S., Demange N.,
XX Arlat M., Woisan A., Robert C., Saurin W., Schiex T.,
XX Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,
XX Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,
XX Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,
XX Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,
XX Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,
XX Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,
XX Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,
XX Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,
XX Siguier P., Thebault P., Whish M., Wincker P., Levy M.,
XX Siguier P., Thebault P., Whish M., Wincker P., Levy M.,
XX Siguier P., Thebault P., Whish M., Wincker P., Levy M.,
XX Siguier P., Thebault P., Whish M., Wincker P., Levy M.,
XX Siguier P., Thebault P., Whish M., Wincker P., Levy M.,
XX Siguier P., Thebault P., Whish M., Wincker P., Levy M.,
XX Siguier P., Thebault P., Whish M., Wincker P., Levy M.,
XX Siguier P., Thebault P., Whish M., Wincker P., Levy M.,
XX Siguier P., Thebault P., Whish M., Wincker P., Levy M.,
XX Siguier P., Canual P., Whish M., Wincker P., Levy M.,
XX Siguier P., Canual P., Whish M., Wincker P., Levy M.,
XX Siguier P., Canual P., Whish M., Wincker P., Levy M.,
XX Siguier P., Canual P., Whish M., Wincker P., Levy M.,
XX Siguier P., Canual P., Whish M., Wincker P., Levy M.,
XX Siguier P., Canual P., Whish M., Wincker P., Canual P., Canual P., Canual P., Canual P., Canual P., Canual P., Canual P., Canual P., Canual P., Canual P., Canual P., Canual P., Canual P., Canual P., Canual P., Canual P., Canual P., Canual P., Canual P., Canual P., Canual P., Canual P., Canual P., Canual P., Canual P., Canual P., Canual P., Can
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Best Local Similarity
Matches 324; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2003 (Tremblylenetetrahydrofolate reductase exidoreductase protein (EC 1.7.99.5).
METF OR RSC0091 OR RSC02264.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                     Oxidoreductase;
SEQUENCE 276 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ralstonia solanacearum (Pseudon
Bacteria; Proteobacteria; beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARVIVTQLEYDTDIELKEVNDCRQIGITCPIVPGIMPINNYKGFIRMTGECKTKIPADIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WSRGWASLYPEDEASRKLYEEVGGSHFLVSLVDNDYINGDLFAVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QLEKINTKGFLTINSQPAVNGEKSDSPTVGWGGPGGYVYQKAYVEFFCSKEKLDALVDKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KVSRSLPWRRPANVFRVKEDVRPIFWANRPKSYISRTIGWDQYPHGRWGDSCNPSYGALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AALEPIKDNEEAVKAYGIHLGTEMCKKILAHGIKTLHLYTLNMEKSALAILMNLGLIEES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WTRGWGCMFPEGDSSRELLEKVQKTYYLVSLVDNDYVQGDLFAAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KAFPSLTYIAVNKDGETFSNISPNAVNAVIWGVFPGKEIIQPTVVDHASFWVWKDEAFEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DHQFTRPRGRGKKLQEEWAVPLKSVEDISERFTNFCQGKLTSSPWSELDGLQPETKIIDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KDRTSLTYMAVNKDGSWKSNVGQTDVNAVTWGVFPAKEIIQPTIVDPVSFNVWKDEAFEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QLVNINQKGFLTINSQPAVNGEKSDSPTVGWGGPGGYVYQKAYLEFFCAKEKLDQLIEKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KVSRPLPWRPATNVFRVKEDVRPIFWANRPKSYLKRTLGWDQYPHGRWGDSRNPSYGALT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AALDPIKDNEEAVROYGIHLGTEMCKKILATGIKTLHLYTLNMDKSAIGILMNLGLIEES
                                                                                           47; Conser
                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                     AA,
                                                                                                                                                                                                                              Complete proteome
AA; 30770 MW; 3A
                                                                                                                          11.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Pseudomonas solanacearum).
ia; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1762; Di
Pred. No. 2.4e
35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35;
                                                                                   Score 246; DB 16;
Pred. No. 6.4e-13;
23; Mismatches 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                 3A5DCB860DB63A2B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 10;
2.4e-142;
nes 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA
                                                                                           46;
                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
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                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60
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RY SERAIN-ANCO 15692 / PAO1;

XX MEDLINE-20407337; PubMed=10984043;

XX MEDLINE-2040737; Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

XX MICKEY M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

XX Merchan R.L., Goltry L., Tolentino E., Westbrock-Weadman S., Yuan Y.,

XX Merchan R.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

XX Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

XX Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

XX Merchan R.L., Hancock R.S., Wu Z., Paulsen I.T.,

XX Merchan R.L., Hancock R.E.W., Lory S., Olson M.V.;

XX Merchan R.L., Hancock R.E.W., Lory S., Olson M.V.;

XX Merchan R.L., Hancock R.E.W., Lory S., Olson M.V.;

XX Merchan R.L., Hancock R.E.W., Lory S., Olson M.V.;

XX Merchan R.L., Hancock R.E.W., Lory S., Olson M.V.;

XX Merchan R.L., Hancock R.E.W., Lory S., Olson M.V.;

XX Merchan R.L., Hancock R.E.W., Lory S., Olson M.V.;

XX Merchan R.L., Hancock R.E.W., Lory S., Olson M.V.;

XX Merchan R.L., Hancock R.E.W., Lory S., Olson M.V.;

XX Merchan R.L., Hancock R.E.W., Lory S., Olson M.V.;

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XX Merchan R.L., Hancock R.E.W., Lory S., Olson M.V.;

XX Merchan R.L., Hancock R.E.W., Lory S., Olson M.V.;

XX Merchan R.L., Hancock R.E.W., Lory S., Olson M.V.;

XX Merchan R.L., Hancock R.E.W., Lory S., Olson M.V.;

XX Merchan R.L., Hancock R.E.W., Lory S., Olson M.V.;

XX Merchan R.L., Hancock R.E.W., Lory S., Olson M.V.;

XX Merchan R.L., Hancock R.E.W., Lory S., Olson M.V.;

XX Merchan R.L., Hancock R.E.W., Lory S., Olson M.V.;

XX Merchan R.L., Hancock R.L., Hancock R.L., Hancock R.L., Hancock R.L., Hancock R.L., Hancock R.L., Hancock R.L., Hancock R.L., Hancock R.L., Hancock R.L., Hancock R.L., Hancock R.L., Hancock R.L., Hancock R.L., Hancock R
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Q9A6F4;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat 5,10-methylenetetrahydrofolate reductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2002 (TrEMBLrel. 16, Last sequence update) 5,10-methylenetetrahydrofolate reductase.
METF OR PA0430.
               SEQUENCE FROM N.A.
STRAIN=ATCC 19089 / CB15;
MEDLINE=21173698; PubMed=11259647;
                                                                                                                                                                                                                          Caulobacter crescentus. Bacteria; Proteobacteria;
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-JUN-2002 (TrEMBLrel. 21,
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InterPro; IPRO03171; Mehydrof_re
Pfam; PF02219; MTHFR; 1.
TIGREAMS; TIGRO0676; fadh2; 1.
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43; Conserv
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Pred. No. 7.8e
22; Mismatches
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7.8e-11;
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Matches 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-MAR-2002 (TrEMBLrel. 20,
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InterPro; IPR003171; Mehydrof_redctse
Pfam; PF02219; MTHER; 1.
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44; Conservative
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314 AA;
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Last annotation update)
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1.1e-10;
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Q1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-DEC-2002 (TrEMBLrel. 21, Last annotation update)
Probable 5,10-methylenetetrahydrofolate reductase oxidoreductase
protein (EC 1.7.99.5).
METF OR R02199 OR SMC01843.
                                                                                                                                                                                                                                                                                                   Renard C., Thebault P., Vandenbol M., Weidner S., Galibert I "Analysis of the chromosome sequence of the legume symbiont Sinorhizobium meliloti strain 1021."; Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001). EMBL; AL591789; CAC46778.1; -.
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EMBL; AE003948; AAF83931.1; -.
HSSP; P00394; 1B5T.
                                                                                                                                                                                                                                  InterPro; IPR004620; Fadh2_bact.
InterPro; IPR003171; Mehydrof_re
Pfam; PF02219; MTHFR; 1.
TIGRPAMS; TIGR00676; fadh2; 1.
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Bacteria; Proteobacteria; alpha subdivision;
Rhizobiaceae; Sinorhizobium.
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Pfam; PF02219; MTHFR; 1.
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240 PIDDQPEERFREAAHIAAEQVADLVRRGVSDFHLYTMNRPQLITAVCELMG
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                                                                                      5 VTQLFYDTDIFLKFVNDCRQIGITCPIVPGIMPINNYKGFIRMTGFCKTKIPADIMAALE 64
                                 PIKDNEEAVKAYGIHLGTEMCKKILAHGIKTLHLYTLNMEKSALAILMNLG
                                                                  LTQFFFDNDDFERYLERVRRAGIAIPIVPGILPINNLTQVQKFAGLCGARVPESIVSRLG
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39; Conser
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Pred. No. 1e-08;
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May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam
"Complete genomic sequence of Pasteurella multocida
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
EMBL; AE006058; AAKO2319.1; -.
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Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                  Complete proteome. SEQUENCE 295 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tetra hydrofolate reductase MTR1.
                                                                                                                                                                                                                                                                                                                               TIGRFAMs; TIGR00676; fadh2; 1.
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InterPro; IPR003171; Mehydrof_re
                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-PM70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          METF OR PM0235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003171; Mehydrof_redctse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN-ATCC 28383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                094090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124
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DPIKDDDELVRDIGTNLIVE-CVKIARQWLRSHLHIYTMNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IITQMFYDVDNFINWCSQVRAAGMDLPIIPGIMPITTYAAFLRRAQWANLH-PSTFLVRL 123
                                                                                                                                                                                                                                                                                                                                                               PF02219; MTHFR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           P00394; 1B5T
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                                                                                                                                            Similarity
38; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomycetaceae;
                                                                                                                                                                                                                                                                     33064 MW;
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                                                                                                                                                                                                                                                                                                                                                                                        Mehydrof_redctse
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17,
21,
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he EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22;
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Last sequence update)
Last annotation update)
                                                                                                                                         Score 196; DB
Pred. No. 1.4e
21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
Last sequence up
Last annotation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 197.5; DB 3 Pred. No. 4.3e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                  7BC42A982E03AFEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5B412E4B893D069C CRC64;
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                                                                                                                                         DB 16;
L.4e-08;
hes 57;
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                                                                                                                                                                                                  Length 295;
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James K.D., Parkhill
Submitted (AUG-1999)
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Q9S2V3; Q1-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence
01-JUN-2002 (TrEMBLrel. 21, Last annotation)
5,10-methylenetetrahydrofolate reductase.
METF OR SCO2103 OR SC4A10.36C.
                                                                                                                                                                InterPro; IPR003171; Mehydrof_redctse.
Pfam; PF02219; MTHFR; 1.
TIGRRAMS; TIGR00676; fadh2; 1.
SEQUENCE 307 AA; 33295 MW; 95A09BS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kinashi H., Hopwood D.A.;
Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-98(1996).
                                                                                                                                                                                                                                                  "Complete genome sequence of the model coelicolor A3(2)."; Coelicolor A1(2)."; Nature 417:141-147(2002).

EMBL; AL109663; CAB52012.1; -.
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Submitted (AUG-1999) 1
                                                                                                                                                                                                                                       HSSP; P00394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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InterPro; IPR004620; Fadh2_bact
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250
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                        PIKDNEEAVKAYGIHLGTEMCKKILAHGIKTLHLYTLNMEKSALAILMNLGL
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the EMBL/
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EMBL/GenBank/DDBJ
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Last annotation updat
                                                                                                                         Score 193;
Pred. No. 2
                                                                                                                                                                   95A09B9FE936D523 CRC64;
                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomycetaceae; Streptomyces.
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                                                                                                          DB 16;
2.6e-08;
nes 53;
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301
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RESULT
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Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M. Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
                                                         Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
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InterPro; IPR003171; Mehydrof_redctse.
Pfam; PF02219; MTHER; 1
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Nature 413:848-852(2001).
EMBL: AL627279; CAD09516 1; -.
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Escherichia coli O157:H7.
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Best Local 9
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                                                                                                                                                                                                                                                                                                          EMBL; AE005625; AAG59142.1; -.
EMBL; AP002567; BAB38293.1; -.
InterPro; IPR004620; FaAh2_bact.
InterPro; IPR003171; Mehydrof_redctse.
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TIGRFAMs; TIGR00676; fadh2; 1.
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Nature 409:529-533(2001).
[2]
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                                                                                                                                                                                                                                                             Complete proteome.
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                                                                                                                         181 ITQFFFDVESYLRFRDRCVSAGIDVEIIPGILPVSNFKQAKKFADMINVRIPAWMAQMFD
                                                            241 GLDDDAETRKLVGANIAMDMVKILSREGVKDFHFYTLNRAEMSYAICHTLGV
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GenCore version Copyright (c) 1993 - 2003 5.1.3 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

February 14, 2003, 23:08:27; Search time 2159 Seconds

(without alignments)
3060.564 Million cell updates/sec

Run on:

Perfect score: Sequence: US-09-720-451-6
2187
1 ARVIVTQLFYDTDIFLKFVN.....VSLVDNDYINGDLFAVFADF 408

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext 16154066 seqs, 8097743376 residues 7.0

Searched:

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq Maximum DB seq length: 0 length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Command line parameters:
-MODEL=frame+\_p2n.model -DEV=x1h

-Q=/cgn2\_1/USPTO\_Spool/US09720451/runat\_05022003\_074816\_2604/app\_query.fasta\_1.583
-DB=EST -QFMT=fastap -SUFFIX=rst -MINARCH=0.1 -LOOPEXT=0
-UNITS=bits -START1 -END-1 -MARIX=blosum62 -TRANS-human40.cdi -LIST=45
-DCCALIGN=200 -THR\_SCORE-pct -THR\_MAX=100 -THR\_MIN-0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN-0 -MAXLEN-200000000
-USER-US09720451\_@CGN\_11\_763\_@runat\_0502503\_074816\_2604 -NCPU=6 -ICPU=3
-NO\_XLPXY -NO\_MMAP -LARGEQUERY -NEG\_SCORES-0 -WAIT -LONGLOG -DEV\_TIMEOUT=120
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPDP=10 -XGAPDEXT=0.5 -FGAPDEXT=7

Database :

YGAPOP=10

-YGAPEXT=0.5 -DELOP=6 -DELEXT=

gb\_est1:\* em\_estpl:\* em\_estov:\* em\_estmu:\* em\_estba:\*
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gb\_est2:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

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HTC 25-MAY-2002

RESULT 1
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LOCUS
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Zea mays PCO119715 mRNA AY109096 AY109096.1 GI:21212506 HTC. Zea mays. sequence. 2423 bp mRNA

Zea mays

Zea mays

Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 2423)

Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S.,

Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.

REFERENCE

AUTHORS

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Overgo
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Direct Submission
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$\text{321 c} 619 \text{ } 648 \text{ } 5 \text{ others}$
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/db_xref="MaizeDB:636961"
/db_xref="taxon:4577"
/clone="PCO119715"
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                       Department of Plant Biology
University of Minnesota
220 BioSci Center, 1445 Gor
Tel: 612 624 2755
                                                                            Unpublished (2002)
Contact: VandenBosch
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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         BioSci Center, 1
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kvandenb@cbs.umn.edu
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/tissue_type="mixed tissues"
/dev_stage="various stages"
/lab_host="XLOLR"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicottyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae
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1100 Bates Street, Houston,
Tel: 713-798-7044
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Contact: Michael A. Grusak
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More information is available
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mgrusak@bcm.tmc.edu
     Ø
in liquid nitrogen. Pod walls were pooled for mRNA extraction. cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing CDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propogated in XLOLR cells."
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                                                                                                                                                                                                                                               /tissue_type="immature pod walls"
/dev_stage="Immature pods, ranging in age from
days after pollination"
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                                                                                                                                                                                                                                                                                       256
                                                                                                                                                                                                                                                                                       Ø
                                                                                                                                                                                                                                                                                  Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/gppages/bgn/31/cover.html)" 216 c 241 g 219 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 California, Riverside (Choi). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plants were grown in the greenhouse at the University of California, Riverside (Fenton, SJ Close, TJ Close). Whole spikes with awns trimmed were collected at 20 DAP (Fenton
                                                                                                                                                                                                                                                                                                                                                                                        http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders Also
see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ). Total RNA was prepared, poly(A) RNA was purified, one
primary unamplified cDNA library was made, and I million
pfu were in vivo excised to give pBluescript SK(-) cDNA
phagemids in the TJ Close lab at the University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Hordeum vulgare
HVcDNA0010 (20 DAP)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                preparation and sequence analysis see
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/db_xref="taxon:4513"
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EST.
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HVSMEk0023I06f Hordeum vulgare testa/pericarp EST library
HVcDNA0013 (normal) Hordeum vulgare cDNA clone HVSMEk0023I06f, mRNA
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Kannangara,G., von Wetstein,D., Akhunov,E., Chin,A., Choi,D.W., Fenton,R.D., Kianian,P., Otto,C., Simons,K., Zhang,D., Begum,D., Frisch,D., Yu,Y.,
                            Spermatophyta; Magnoliophyta; Er
Triticeae; Hordeum.
1 (bases 1 to 823)
Wing p 71-
                                                                       Hordeum vulgare
Eukaryota; Viridiplantae;
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                                                             Embryophyta; Tracheophyta;
a; Poales; Poaceae; Pooideae
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Best Local Similarity:
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                                                 LeuAlaIleLeuMetAsnLeuGlyLeuIleGluGluSerLysValSerArgSerLeuPro
                                                                                                  100 Jordan Hall, (Tel: 864 656 7288 Fax: 864 656 4293
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Clemson University Genomics
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/note="Wector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;

Plants were raised from seeds in a Controlled Environments
growth chamber maintained in continuous light at 180C, and
testa and perioarp were dissected from developing kernels
at Washington State University, Pullman, WA (Kannangara,
von Wetstein). Total RNA was prepared, poly(A) RNA was
purified, one cDNA library was made, and I million pfu
were in vivo excised to give pBluescript SK(-) cDNA
phagemids in the TJ Close lab at the University of
California, Riverside (Akhunov, Chin, Choi, Close, Fenton,
Kianian, Otto, Simons, Zhang). Phagemids were plated and
picked at the Clemson University Genomics Institute (CUGI)
(Begum, Palmer, Frisch, Akkins and Wing). Plasmid DNA
preparations, DNA sequencing and sequence analysis were
performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates
, Rambo, Main). The sequence has been trimmed to remove
vector sequence and contains a minimum of 100 bases of
phred value 20 or above. For more details on library
preparation and sequence analysis see
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)" 187 c 207 g 192 t 1 others
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/db_xref="taxon:4513"
/clone="HVSMEk0023106f"
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/lab_host="TJC121"
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnollophyta; Fabales; Fabaceae; Papilionoideae; Phaseoleae
                           Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
                                                                                           Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna, A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C. Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
                                                                                    Unpublished (1999)
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METHYLENETETRAHYDROFOLATE REDUCTASE; , mRNA sequence.
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LeuGlnProGluThrLysIleIleAsnGluGlnLeuGluLysIleAsnThrLysGlyPhe
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                                                      ArgPheArgLeuTyrCysLeuGlyLysLeuArgSerAsnProTrpSerGluLeuAspGly
                                                                                                    GACAAGAAGCTTGTTGAAGAATGGGCAGTTCCCCTTGAAAAGCATTGAAGATATATGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: est@watson.wustl.edu
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Fax: 314 286 1810
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Coryell." 181 g 180 t
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/note="Vector: pBluescript II SK+; Site_1: EcoRI;
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BQ994876.1 GI:22414411
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                                                                                                            Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
                                                                                                                                                                                                     Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J., Elli:
, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z.,
Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
                                                                                                                                                                                                                                                                                                                       Lactuca sativa
                                                                  belongs to contig
for details.
Plate: QGF8 row:
                                                                                        Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu] belongs to contig QG_CA_Contig1724, see http://cgpdb.uc
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/organism="Lactuca sativa"
/cultivar="L.serriola"
/db_xref="taxon:4236"
/clone="QGF8G21"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IleProAlaAspIleMetAlaAlaLeuGluProIleLysAspAsnGluGluAlaValLys
                                                                                                                                                                                             CAAGCAGAATGGGTGCCTTTGACCAAGTTTGATGATATTTCCGAGAAATTCATGAAG
                                                                                                                                                                                                                                                                TCAAGGACGGGTGGTTGGGAGCAATATCCACATGGGCGTTGGGCGGATTCTTCTAATGCA 422
                                                                                                                                                                                                                                                                                                                                                         SerArgThrIleGlyTrpAspGlnTyrProHisGlyArgTrpGlyAspSerCysAsnPro 174
                                                                                                                                                                                                                                                                                                                                                                                                          TTCCGTCTTAAAGAAGATGTTAGGCCAATTTTTCTGGGCCAATCGTCCAAAGAGCTACATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGATTGGTTGACGAGGCCAAAATTACAAGACCACTTCCATGGAGGAGACCTACTAACCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GlyLeuIleGluGluSerLysValSerArgSerLeuProTrpArgArgProAlaAsnVal 134
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                                                                                                                       TACTGCCTTGGGCAACTAAAAACCAGCCCTTGGTCGGACCTGGATGCGCTTCAGCCAGAG
                                                                                                                                           TyrCysLeuG1yLysLeuArgSerAsnProTrpSerG1uLeuAspG1yLeuG1nProG1u
                                                                                                                                                                                                                         ValGluGluTrpAlaValProLeuLysSerValGluAspIleTyrGluArgPheArgLeu
                                                                                                                                                                                                                                                                                   SerGlnProAlaValAsnGlyGluLysSerAspSerProThrValGlyTrpGlyGlyPro
                                                  ACAAAAATCATCAACGAGGAACTGGCTTCCATCAACCTCAAGGGTTTCCTCACCATCAAC
                                                                      Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cypdb.ucdavis.edu/TAG_IIB=0G_EFGHJ lettuce serriola
TAG_TISSUE=flowers post-fertilized
TAG_SEQ=TGCCATCGGG"
175.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="QG_EFGHJ lettuce serriola"
/lab_host="E.coli"
/note="Vector: pBRcDNASfiAB; The libra:
from 10 different sources of RNA from
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AGCCAACCCGCTGTTAATGGAGCCAAATCTGACTCCCCATCTGTTGGATGGGGCCCCAGCG 722

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JOURNAL COMMENT
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Wylle, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers
, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schur, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available through: ResGen, Invitrogen Corp. 2130

South Memorial Parkway Huntsville, AL 35801 For further information

call: (800)-533-4363 or contact via email: ccu@resgen.com

Insert Length: 1257 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AW830074 631 bp mRNA linear EST 03-DEC-2001 sm22h02.y1 Gm-c1028 Glycine max CDNA clone GENOME SYSTEMS CLONE ID: Gm-c1028-4684 5' similar to SW: MTHR. ARAPH 080585 PROBABLE GM-C1028-4684 5' REDUCTASE ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Shoemaker R/Public Soybean Public Soybean EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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Location/Qualifiers
first-strand synthesis primer was used. An 'anchor' nucleotide (V=A,C, or G) was added to the 3' end of the primer [GAGAGAGAGAGAGAGAGAGAGAGAGTCTGGAG(T)18V] to anchor the primer at the 5' end of the poly(A) tract. After second-strand synthesis, the cDNA ends were filled in with cloned Fru DNA polymerase, ligated to EcoRI adapters and subsequently phosphorylated. The XhoI site within the first-strand synthesis primer was then restricted by digestion with XhoI; all XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500bp cutoff, using GibcoBRL Life Technologies' cDNA size Fractionation column. The column eluent was then ligated into Stratagene's pBluescript II XR Predigested vector
                                                                                                                                                                                                                                                                                            /note-"Vector: pBluescript II XR; Site_1: EcoRI; Site_2: XhoI; The mRNA was isolated from roots of Glycine max 'Supernod' plants generously donated by Dr. Gary Stacey. The seedlings were innoculated with Bradyrhizobium japonicus, strain USDA110 priot to harvest. Stratagene's CDNA synthesis kit (catalog number 200401) was used to synthesize the cDNA. First-strand synthesis was perform with 5-methyl dCTP, hence the ligated cDNA was hemimethylated. A modification of Stratagene's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="GENOME SYSTEMS CLONE ID: Gm-c1028-4684"
/clone_lib="Gm-c1028"
/tissue_type="roots of 'Supernod' plants"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Glycine max"
/db_xref="taxon:3847"
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(pBluescript II SK(+) that has been digested with Ecoland XhoL, and phosporylated by Stratagene). Both the white and blue colonies appear to contain recombinant plasmids with cDNA inserts, based on size (n=25). Thi library was constructed by Dr. Paul Keim and Dr. Virg Coryell."

2 others

114 c 158 g 166 t 2 others Dr. Virginia ECORI the

US-09-720-451-6 (1-408) x AW830074 (1-631) 2 AAAGAAGATGTCCGTCCAATCTTTTGGGCAAATCGTCCAAAAAGCTACATATCAAGGACA AlaValAsnGlyGluLysSerAspSerProThrValGlyTrpGlyGlyProGlyGlyTyr GAAAGTTGAGAAGCAATCCTTGGTCAGAACTAGATGGTCTTCAGCCAGAGACAAAGATA TrpAlaValProLeuLysSerValGluAspIleTyrGluArgPheArgLeuTyrCysLeu LysGluAspValArgProIlePheTrpAlaAsnArgProLysSerTyrIleSerArgThr GluIleIleGlnProThrIleValAspPro 347 LysSerAsnValGlyGlnThrAspValAsnAlaValThrTrpGlyValPheProAlaLys AspLysCysLysAspArgThrSerLeuThrTyrMetAlaValAsnLysAspGlySerTrp IleAsnGluGlnLeuGluLysIleAsnThrLysGlyPheLeuThrIleAsnSerGlnPro AlaLeuSerAspTyrGlnPheMetArgProArgAlaArgAspLysLysLeuValGluGlu 197 GAGATTATTCAAACCAACATTTGTGATCCT AAATCTAATGTGGGTCAAACTGATGTNAATGCTGTGACATGGGGTGTCTTNCCAGCTTAG GATAAATGCAAGGATCGAACATCTTTAACTTATATGGCTGTGAATAAAGACGGGAGCCTG GCTGTCAATGGGGAAAAGTCAGATTCTCCTACTGTTGGCTGGGGTGGACCAGGCGGGTAT GlyLysLeuArgSerAsnProTrpSerGluLeuAspGlyLeuGlnProGluThrLysIle TGGGCAGTTCCCTTGAAAAGCATTGAAGATATATATGAGAGGTTTAGACTGTATTGTCTT GCATTATCTGATTATCAGTTCATGCGGCCACGTGCACGGGACAAGAAGCTTGTTGAAGAA ATAGGATGGGATCAATACCCACACGGGCGTTGGGGTGATTCCTGTAATCCATCATATGGT BE576981 700 bp mRNA linear EST 20-FEB: LO-1588T3 Ice plant Lambda Uni-Zap XR expression library, 0 hous NaCl treatment Mesembryanthemum crystallinum cDNA clone LO-1588 BE576981.1 GI:9826689 sequence. 5.65e-123 1093.00 96.67% 96.19% 49.98% Length: Matches: Mismatches: Indels: Conservative: 631 EST 20-FEB-2001 297 541 481 421 277 361 257 301 237 241 217 181 121 61 hours 1588 5',

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AUTHORS
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                                                                                                 TrpArgArgProAlaAsnValPheArgValLysGluAspValArgProIlePheTrpAla 147
                                                                                                                                                 LeuAlaIleLeuMetAsnLeuGlyLeuIleGluGluSerLysValSerArgSerLeuPro
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                                              AsnArgProLysSerTyrIleSerArgThrIleGlyTrpAspGlnTyrProHisGlyArg 167
                                                                                                                                    TTAGCAATTTTGACGAATCTTGGATTAATTGAAGAATCCAAAATCCAAAGGTCATTACCT
                                                                                                                                                                                                                                    GACAATGATGAGGCCGTGAAGGCCTACGGGATTCACCTCGGAACTGAAATGTGCAAGAAG
           TrpGlyAspSerCysAsnProSerTyrGlyAlaLeuSerAspTyrGlnPheMetArgPro
                                    AATCGTCCAAAAAGTTACCTTACGCGGACAGTTGGATGGGATCAGTACCCACAGGGGCGA
                                                                                    TGGAAACGCCCTGCAAATGTGAACCGCGTTAAAGAAGATGTTCGTCCCATATTTTGGGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1997)
Contact: Cushman JC
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Plate: L0-16
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FORWARD: T7
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/db_xref="taxon:3544"
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Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T., Holtala,J., Upton,J., Craven,M.B., Bowman,C.L., Ahn,S., Ronnir,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni. Generation of ESTs from tomato callus tissue Unpublished (1999)
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Wing, R., Close, T.J., Kleinhofs, A., Wetstein, D., Akhunov, E., Chin, A., (P., Otto, C., Simons, K., Zhang, D.,
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HVSMEk0021017f Hordeum vulgare
                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
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Eukaryota; Viridiplantae;
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inhofs,A., Wise,R., Kannangara,G.,
Chin,A., Choi,D.W., Fenton,R.D.,
Zhang,D., Begum,D., Frisch,D., Yu
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                                                                                                                                     AlaHisGlyIleLysThrLeuHisLeuTyrThrLeuAsnMetGluLysSerAlaLeuAla 109
ATTCTGATGAATCTTGGATTAATAGAGGGAATCCAAGCTTTCAAGAACATTACCTTGGAGG
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Total hq bases = 539
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Tel: 864 656 7288
Fax: 864 656 4293
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38 a 193 c 215 g 195 t 1 others
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Plants were raised from seeds in a Controlled Env
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HVcDNA0013 (normal)"
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                                                                             Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C. Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and Wilson, R.
                                                                                                                                                                                                                                                                                               BEB05904 611 bp mRNA linear EST 06-DEC-2001 ses62h07.y1 Gm-c1062 Glycine max CDNA clone GENOME SYSTEMS CLONE ID: Gm-c1062-1046 5' similar to SW:MTHR.ARAFH 080585 PROBABLE METHYLENETETRAHYDROFOLATE REDUCTASE ;, mRNA sequence.
                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae
public Soybean EST Project Unpublished (1999) (Contact: Shoemacr R/Public Soybean EST Project Public Soybean EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, 1
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High quality sequence stop: 410.
Location/Qualifiers
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Fax: 314 286 1810
Email: est@watson.wustl.edu
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/dev_stage="1 month old"
/lab_host="DH10B"
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/db_xref="taxon:3847"
/clone="texonEySrgmy CLONE ID: Gm-c1062-1046"
/clone_lib="Gm-c1062"
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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EST469531 tomato shoot/meristem Lycopersicon esculentum
cTOF3B13 5' sequence, mRNA sequence.
BG123885
BG123885.1 GI:12624073
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Contact: CUGI
Clemson University Genomics Institute
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Hansen,C., Ronning,C. and Tanksley,S.
Generation of ESTs from tomato shoot/meristem tissue
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                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:4081"
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                                                                                                                                                                                                                                                                                /clone_lib="tomato shoot/meristem"
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                                                                                                                                                                                                                                                                                                                                                /organism="Lycopersicon esculentum"
/cultivar="TA496"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             BE643238 821 bp mRNA C112_8_E11_SP6 Ceratopteris Spore Library CDNA clone Cri2_8_E11 5', mRNA sequence. BE643238 BE643238.1 GI:9960923
                                                                                                                                                        Section of Molecular Cell and Developmental University of Texas Biology Building, Room 16, Austin, TX 78712, Tel: 512 471 4238
                                                                                                                                                                                                                                                             Chatterjee, A., San Miguel, P., Stout, S.C., Banks, J. and Roux, S.J. Expressed sequence tags of cDNA clones from a C. richardii libra Unpublished (2000) Contact: Roux SJ
                                                                                                Plate: Cri2_8
Seq primer: SP6
                                                                                                                      Email: sroux@uts.cc.utexas.edu
Plate: Cri2_8 row: E column:
                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Filicophyta; Filicopsida;
                                                                                                                                                                                                                                                                                                                                                                                                       Ceratopteris richardii.
Ceratopteris richardii
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/organism="Ceratopteris
/cultivar="Brogn"
/db_xref="taxon:49495"
                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                Streptophyta; Embryophyta; Tracheophyta; Filicales; Pteridaceae; Ceratopteris.
                                           richardii"
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Ceratopteris richardii
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                                                                                                                                                                                                                          GAAGGTTTGCAGCCAGAAACTGAAAAAATCAACTCTAAATTAGTAGAGATCAACTCTAAA
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                                                                                                                                                                                                                                                                                                                                                                               TCTCGCAACAAGAAATCCAAGAAGAGTGGGTTGTGCCTTTGAATGACATCAACGACATT
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                    SerLysGluLysLeuAspAlaLeuValAspLysCysLysAspArgThrSerLeuThrTyr 308
                                                                                            ValGlyTrpGlyGlyProGlyGlyTyrValTyrGlnLysAlaTyrValGluPhePheCys
                                                                                                                                                                    GlyPheLeuThrILeAsnSerGlnProAlaValAsnGlyGluLysSerAspSerProThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlyAspSerCysAsnProSerTyrGlyAlaLeuSerAspTyrGlnPheMetArgProArg
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/clone_lib="ceratopteris Spore Library"
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/dev_stage="20 hours after germination initiation"
/note="Yector: pcMYSPORT6; EST sequence from cDNA library constructed from mRNA isolated from C.
richardii spores that had developed for 20 hours after their germination had been initiated by white light."
a 162 c 187 g 214 t 2 others
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public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Public Soybean EST Project
Washington University School of Medicine
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnollophyta; Fabales; Fabaceae; Papilionoideae; Phaseoleae
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High quality sequence stop: 414.
Location/Qualifiers
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314 286 1810
                                                                                                                             /note="Tvector: pBluescript II SK+; Site_1: ECORI; Site_2: XhoI; The cDNA library was constructed from mRNA isolated from germinating shoots of 3 day old seedling for the cultivar williams 82. The seedlings were germinated in a growth chamber using germination paper in a solution containing 100ppm auxin. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated CDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Glycine max"
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/clone="GENOME SYSTEMS CLONE ID: Gm-c1067-1734"
/clone_lib="Gm-c1067"
/clone_type="Germinating shoot, 3 day old seed treatment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Box 8501,
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Search completed: February Job time : 2170 secs	Db	Qy	Dр	Qy	Db	Qy :	Дb	Qy :	Db	Qy	뭥	Qy	<b>Db</b> 1	Qy	рь	Qy	Db	Qy	망	Qy	US-09-720-451-6	DB:
e cor	544	183	484	163	424	143	364	123	304	103	244	83	184	63	124	43	64	23	4	w	20-	
mple : 21	CAG	Gln	TAC	Tyr	CCA	Pro	TCT	Ser	ATG	- t	GAA	Glw	TTA	Leu	GGC	G1y	cec	Arg	CTG	Val:	451	
ted 70 s	TIC	Phel	CCAC	ProF	ATC	Ilei	AGG	Args	GAGA	GluI	ATGT	Metc	GAGC	Gluf	TTTA	PheI	CAAA	= 12 m	ATTG	[]eV		
secs	TIGC	/etA	ATG	11SG	TTT	heT	CCT	erL	A A	Sskr	GCA	YSL	CTA	FOI	TCC	leA:	TIG	1eG	TCAC	alT!	1-4(	
brue	GGC	rgPı	GGCG	1yAz	GGGC	rpAl	TACC	euPr	CTGC	erAl	AAAA	ysLy	TCAA	leLy	GCAT	rgMe	SAAT	LyIl	CCCA	nrG1	(8)	
ary	ACG	OAr	TTG	gTr	AAA	aAs	TTG	- OI	ATT	aLe	GAT	SIL	GGA	SAS	GAC	- ti	AAC	eīb.	ATT	nLeu	× BI	12
15,	TGCA	gAla	GGGT	pG1y	TCGA	nArg	3AGA	pArg	3GCA	ıAla	TTTA	eLeu	CAAT	Asn	rGGA	cGly	TGT	Cys	TTT	ıPhe	071	
2003,	cee	Arg/	GAT	Asp	CCA	Prol	CGCC	Argi	ATAC	Ilei	GCTC	Alai	GAAC	Gluc	TTTT	Phec	CCTA	Prol	TATG	TyrA	(1-408) x BF071278 (1-	
	BACA	AspL	CCT	SerC	AAA	yss	cre	roA	TAA	euM	ATG	IisG	AAG	LUA	GCA	ysL	TTG	1ev	ATA	spT]	(1-	
00:51:19	AGA	ysĽ)	GTA	ys As	GCTA	erTy	CAA	laAs	TGAA	etAs	GAAT	1yI1	CTGT	laVa	AAAC	ysTh	FACC	alpr	CGGA	nrAs	588)	Gaps:
1:19	GCT	/sLe	TCC	inPr	CAT	711	TGT	nVa	CCT	nLe	TAAC	eLy:	CAAC	LLys	AAAC	rLys	TGGZ	0613	TAT	PILE		8
	CAGTTCATGCGGCCACGTGCACGGGACAAGAAGCTTGTTGAAGAA	GlnPheMetArgProArgAlaArgAspLysLysLeuValGluGlu	TACCCACATGGGCGTTGGGGTGATTCCTGTAATCCATCATATGGTGCATTATCTGATTAT	TyrProHisGlyArgTrpGlyAspSerCysAsnProSerTyrGlyAlaLeuSerAspTyr	ATCA	ProllePheTrpAlaAsnArgProLysSerTyrIleSerArgThrIleGlyTrpAspGln	TIC	SerArgSerLeuProTrpArgArgProAlaAsnValPheArgValLysGluAspValArg	GGC	MetGluLysSerAlaLeuAlaIleLeuMetAsnLeuGlyLeuIleGluGluSerLysVal	ACA	GluMetCysLysLysIleLeuAlaHisGlyIleLysThrLeuHisLeuTyrThrLeuAsn	GCT	LeuGluProIleLysAspAsnGluGluAlaValLysAlaTyrGlyIleHisLeuGlyThr	GGCTTTATCCGCATGACTGGATTTTGCAAAACAAAGATACCAGCTGACATTATGGCTGCT	GlyPheIleArgMetThrGlyPheCysLysThrLysIleProAlaAspIleMetAlaAla	CGCCAAATTGGAATAACGTGTCCTATTGTACCTGGAATTATGCCCCATTAATAATTACAAG	ArgGlnIleGlyIleThrCysProIleValProGlyIleMetProIleAsnAsnTyrLys	TIC	ValIleValThrGlnLeuPheTyrAspThrAspIlePheLeuLysPheValAsnAspCys		
	GAAG	Gluc	TATO	Tyre	AGG	Argī	cere	Argv	CTAA	LeuI	ITGC	LeuH	FATG	TyrG	CAG	ProA	TGC	letp	TCA	euL		
			GTG	lyA	CCA	- hr	TTA	alL	TTG	leG	ATC	isLe	GAA	lyI	CTG	laAs	CCAI		AATI	ysPh		0
	588	197	CATT	laLe	rAGG	leG1	AAGA	/sGl	AGA	LuGl	TTA	euTy	TCA	ені	CAT	  	TAA	-eAs	TGT	leVa.		
			ATC	uSe:	ATG	YTr:	AGAI	uAsp	GTCC		TAC	rThr	CCTG	sLev	TATG	eMet	TAAT	nAsn	SAAC	lAsn		
			IGAT	cAsp	GAT	Asp	GTC	Val	AAA	Lys	CTA	Leu	GGA	G1y	GCT	- Ala	TAC.	Tyr.	GAC	Asp		
			TAT	Tyr	CAA	n19	CGT															
			543	182	483	162	423	142	363	122	303	102	243	82	183	62	123	42	63	22		

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Command line parameters:

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-MODEL-frame-p2n.model -DEV=xlh
-Q-/G9n2_1/USPTO_Spool_US9720451/runat_05022003_074809_2374/app_query.fasta_1.583
-DB-N_Geneseq_101002 -OFMT=fastap -SUFFIX=rng -MINNATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=biosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE-LOCAL -OUTFMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN-0 -MAXLEN-200000000
-USER-US09720451_@CGN_1_1_0_@runat_05022003_074809_2374 -NCPU=6 -TCPU=3
-NO_XIDXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Ygapop 10.0 , Ygapext
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                 N_Geneseq_101002:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being pu and is derived by analysis of the total score distribution. printed,

EP1033405-A2

## SUMMARIES

Result No.	ult No.	Score	% Query Match	Length	BB	ID	Description
;	-	83	ω :	2	21	AAC43311	Arabidopsis thalia
	N	8 5	.ω	94	21	AAC49168	
	د ۵	$\sigma$	54.0	o u	٦ <u>۲</u>	AAC3696/	
	OI I	866		558	21	AAZ50061	Soybean 5,10-methy
	σ	7	4	2187	22	AAC91206	Human methylenetet
	7	7	44.8	2219	17	AAT09689	methylene-t
	8	7	4	2219	22	AAD20463	
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	14	979	44.8	2220	24	ABK13540	Human methylenetet
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	18	979	44.8	2220	2 4	ABK13546	Human methylenetet
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3	7 4	150	7.2	COOT	) K	AAF / 2089	Corynebacterium gi
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## ALIGNMENTS

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RESULT 1
AAC43311
                                                  Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                                   Arabidopsis thaliana DNA fragment SEQ ID NO:
                                                                                                                         17-OCT-2000 (first entry)
                                                                                                                                                                       AAC43311 standard; DNA; 1821
                              Arabidopsis thaliana
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r	90S-01	905-01	9US-01	9US-01	905-01	9US-01	9US-01:	9us-01:	9US-01:	9US-01	9US-01	9US-01:	9US-01	9US-01	905-01	9US-01	9US-01:	9US-01:	9US-01:	908-01	905-01	9US-01	9US-01	908-01	9US-01	9US-01:	908-01	908-01	9US-01	9US-01:	9US-01:	9US-01:	905-01	9US-01:	9US-01	9US-01:	9US-01	9US-01	9US-013	9US-01:	908-013	905-0129845 905-0130077	9US-01	90S-01;	9US-01	9US-01;	9US-01	99US-0121825. 99US-0123180.	2000EP-0301439.	
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AsnGlyAspLeuPheAlaValPheAlaAsp
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AATGGTGACATATTCGCGGTCTTTGCTGAT
                                                                                       GlyLysLeuArgSerAsnProTrpSerGluLeuAspGlyLeuGlnProGluThrLysIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides a novel method of estimating the susceptibility of an individual to a developmental disorder using genetic and environmental variables. The method can be used in the diagnosis, prevention and treatment of disorders such as schizophrenia, spina bifidately cystica, Tourette's syndrome, bipolar illness, autism, conduct disorders, attention deficit disorder, obsessive compulsive disorder, chronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  multiple tic syndrome and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diagnosing a developmental disorder, e.g. schizophrenia, by forming datasets (DS) of genetic (e.g. genotypes of folate metabolism alleles) and environmental variables affecting an individual and then comparing these DS with reference DS -
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AACCTGGTGGACAATGACTTCCCACTGGACAACTGCCTCTGGCAGGTGGTGGAAGAC
                               SerLeuValAspAsnAspTyr---IleAsnGlyAspLeuPheAlaValPheAlaAsp 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human methylene:tetra:hydro:folate reductase cDNA probe - for detection of sequence abnormalities in methylene:tetra:hydro:folate reductase e.g. in cardiovascular, neurological or folic acid metabolism disorders
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                                                         AACCTGGTGGACAATGACTTCCCACTGGACAACTGCCTCTGGCAGGTGGTGGAAGAC
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US-09-720-451-6 (1-408) x AAD20463

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Query Match:
                         Percent Similarity:
Best Local Similarity:
                                                                                 Alignment
                                                                                                                                    5-methylenetetrahydrofolate, a co-substrate for methylation of homocysteine to methionine. The invention provides potential therapy for individuals with MTHFR deficiency. The non allele-specific antisense nucleic acids are useful for treating, stabilising or preventing cancer, particularly breast carcinoma, colon carcinoma, colorectal carcinoma, lung cancer, brain cancer, pancreatic cancer, kidney cell cancer, neuroblastoma, glioma and leukaemia. MTHFR cDNA probe is used in gene therapy. The present sequence is human methylenetetrahydrofolate reductase (MTHFR) protein cDNA #2. Human MTHFR gene is mapped to chromosome 1p36.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 200
P-PSDB;
                                                                                                                                                                                                                                                                     The invention relates to a non allele-specific antisense nucleic acids, which binds to methylenetetrahydrofolate reductase (MTHFR; EC 1.5.1.20) nucleic acids and inhibits MTHFR protein expression in a mammal. MTHFR catalyses the NADPH-linked reduction of 5,10-methylenetetrahydrofolate to
                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                               New antisense nucleic acids, which are methylenetetrahydrofolate reductase inhibitors, useful for treating, stabilizing or preventing cancer, e.g. breast carcinoma, colon carcinoma, colorectal carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; methylenetetrahydrofolate reductase; MTHFR; gene therapy; glioma; antisense therapy; EC 1.5.1.20; chromosome 1p36.3; cancer; kidney cell; pancreas; lung; brain; cytostatic; colon carcinoma; breast; colorectal; neuroblastoma; leukaemia; ss.
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(MTHFR) protein"
/EC_number= "1.5.1.20"
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                                                               Query Match:
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Best Local Similarity:
                                                                                                                                                                                       This sequence encoding human MTHFR has been localised to chromosome 1936,3. It may be used for the construction of DNA probes which may be used for the identification of sequence abnormalities in patients with severe or mild MTHFR deficiency. The resulting probe may also be used in gene therapy to produce the MTHFR protein.
                                                                                                                                                                                                                                                                                               Human methylene:tetra:hydro:folate reductase cDNA probe - for detection of sequence abnormalities in methylene:tetra:hydro:folate reductase e.g. in cardiovascular, neurological or folic acid metabolism disorders
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TTCATGTTCTGGAAGGACGAGGCCTTTGCCCTGTGGATTGAGCGGTGGGGAAAGCTGTAT
                                 PheAsnValTrpLysAspGluAlaPheGluIleTrpSerArgGlyTrpAlaSerLeuTyr
                                                                     ACTTGGGGCATCTTCCCTGGGCGAGAGATCATCCAGCCCACCGTAGTGGATCCCGTCAGC
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cDNA probe for the human methylenetetrahydrofolate reductase (MTHFR), useful in gene therapy and for diagnosing or treating MTHFR deficienc which is associated with cardiovascular disorders or cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cardiovascular disorder; cancer; neuroblastoma;
colorectal carcinoma; osteoporosis; neural tube defect;
neurological disorder; gene therapy; diagnosis; chromosome 1p36.3;
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Best Local Similari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC methylenetetrahydrofolate reductase (MTHFR, see AAY96186), an enzyme CC matalysing the NADPH-linked reduction of 5,10-methylenetetrahydrofolate CC to 5-methyletrahydrofolate, a co-substrate for methylation of 5-methyletrahydrofolate, a co-substrate for methylation of CC bomocysteine to methionine. To identify human MTHFR CDNA, PCR CC primers based on the porcine sequence were used to screen a human CC liver lambda-gt10 cDNA library by PCR. A 1266 bp fragment was CC obtained, and this was used to screen a human colon carcinoma cDNA CC library to obtain the 2.2 kb clone. The MTHFR gene (see AAA50634) CC maps to chromosome 1p36.6. A cDNA probe for human MTHFR, which CC severe or mild MTHFR sequence abnormalities in individuals with CC severe or mild MTHFR sequence abnormalities may comprise CC used to identify MTHFR sequence abnormalities may comprise CC used to T, 764C to T, 792+1G to A, 482G to A, 559C to T, 677C to CC T, 692C to T, 702+1G to A, 985C to T, 1015C to T, 1081C CC T, 692C to T, 702+1G to A, 985C to T, 1015C to T, 1081C CC T, 692C to T, 0015C and 1317T to C. MTHFR deficiency may be associated CC with a cardiovascular disorder, cancer (especially neuroblastoma or CC clorectal carcinoma), osteoporosis, neural tube defect in an CC colorectal carcinoma), osteoporosis, neural tube defect in an CC colorectal carcinoma) associated disorders, and other disorders CC treating MTHFR deficiency by gene therapy or by administration of CC treating MTHFR protein. Cancer can be treated by inhibiting MTHFR gene CC expression or MTHFR protein activity, or by administering an agent CC that modifies MTHFR gene expression.
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TrpAspGlnTyrProHisGlyArgTrpGlyAspSerCysAsnProSerTyrGlyAlaLeu
                                                                AspValArgProIlePheTrpAlaAsnArgProLysSerTyrIleSerArgThrIleGly
                                                                                                                          GACCCC - - - AGGCGTCCCCTACCCTGGGCTCTCAGTGCCCACCCCAAGCGCCGAGAGGAA
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                                                                                                                                   Human; methylenetetrahydrofolate reductase; MTHFR; gene therapy; glioma; antisense therapy; EC 1.5.1.20; chromosome 1p36.3; cancer; kidney cell; pancreas; lung; brain; cytostatic; colon carcinoma; breast; colorectal;
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                                                                                                                                                                                           Human methylenetetrahydrofolate reductase (MTHFR) protein cDNA #1.
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/*tag= a
/product= "Human
(MTHFR) protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity: y Match:
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GCCGTGAGCCTGTGCCAGGAGCTTCTGGCCAGTGGCTTGGTGCCAGGCCTCCACTTCTAC
                                                                                                     GACGTGATTGAGCCAATCAAAGACAACGATGCTGCCATCCGCAACTATGGCATCGAGCTG
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09-APR-2002

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                              alcohol or drug intoxication, postinfection psychosis, postpartum psychosis, senile psychosis, traumatic psychosis and acute idiopathic psychosis illnesses. A new pharmaceutical composition is used for treating amyotrophic lateral sclerosis, anxiety, dementia, depression, epilepsy, Huntington's disease, migraine, demyelinating disease, multiple sclerosis, pain, Parkinson's disease, schizophrenia, psychoses, or stroke. Deficiency may be associated with diseases including cardiovascular disorders, cancer (e.g. neuroblastoma and colorectal carcinoma), osteoporosis, metabolism endocrine disease, inborn errors of metabolism, inflammation, immune disorders, neoplastic disease and renal disease. This sequence encodes human methylenetetrahydrofolate reductase (WTHFR) which maps to chromosome 1p36 (EC number 1.5.1.20), assertibed in the method of the inventions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           anticonvulsant; cerebroprotective; amyotrophic lateral sclerosis; anxiety; dementia; depression; epilepsy; Huntington's disease; migraine; demyelinating disease; multiple sclerosis; pain; Parkinson's disease; psychosis; stroke; cardiovascular disorder; cancer; osteoporosis; metabolic disease; endocrine disease; inboarn error of metabolism; inflammation; immune disorder; human; inboarn error of metabolism; inflammation; immune disorder; human;
                                                                                                                                                                                                                                                                                                                                                                                           or a risk for or propensity to psychosis in a subject comprising determining the presence of a heterozygous methylenetetrahydrofolate reductase (MTHFR) mutant allele in a nucleic acid sample obtained from subject. The method is useful for diagnosing subjects at risk of, or suffering from a psychosis, particularly schizophrenia but includes manic-depressive disease, organic psychotic disorders, psychosis in
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               ThrTrpGlyValPheProAlaLysGluIleIleGlnProThrIleValAspProValSer
                                              CTTGTCAATGTGAAGGGTGAAAACATCACCAATGCCCCTGAACTGCAGCCGAATGCTGTC
                                                                           AlaValAsnLysAspGlySerTrpLysSerAsnValGlyGlnThrAspValAsnAlaVal
                                                                                                                                        GluLysLeuAspAlaLeuValAspLysCysLysAsp---ArgThrSerLeuThrTyrMet
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The invention describes a method of diagnosing a psychosis in a subject or a risk for or propensity to psychosis in a subject comprising determining the presence of a heterozygous methylenetetrahydrofolate reductase (MTHFR) mutant allele in a nucleic acid sample obtained from subject. The method is useful for diagnosing subjects at risk of or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neuroprotective; tranquiliser; nootropic; antidepressant; anticonvulsant; cerebroprotective; amyotrophic lateral sclerosis; anxiety; dementia; depression; epilepsy; Huntington's disease; midraine; demyelinating disease; multiple sclerosis; pain; Parkinson's disease; psychosis; stroke; cardiovascular disorder; cancer; osteoporosis; metabolic disease, endocrine disease; inborn error of metabolism; inflammation; immune disorder; human; neuroblastoma; colorectal carcinoma; neoplastic disease; renal disease; EC number 1.5.1.20; mutant.
                                                                                                 Claim 4;
                                                                                                                                         Diagnosing subjects at risk for or suffering from a psychosis, particularly schizophrenia comprises determining the presence of a heterozygous methylenetetrahydrofolate reductase mutant allele in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC suffering from a psychosis, particularly schizophrenia but includes CC manic-depressive disease, organic psychotic disorders, psychosis in CC alcohol or drug intoxication, postinfection psychosis, postpartum CC psychosis, senile psychosis, traumatic psychosis and acute idiopathic CC psychotic illnesses. A new pharmaceutical composition is used for CC treating amyotrophic lateral sclerosis, anxiety, dementia, depression, CC epilepsy, Huntington's disease, migraine, demyelinating disease, multiple CC sclerosis, pain, Parkinson's disease, schizophrenia, psychoses, or CC stroke. Deficiency may be associated with diseases including CC cardinowascular disorders, cancer (e.g. neuroblastoma and colorectal CC carcinoma), osteoporosis, metabolic or endocrine disease, inborn errors CC of metabolism, inflammation, immune disorders, neoplastic disease and CC contiled of has been altered to produce a mutant allele, described in the approach of the invention altered to produce a mutant allele, described in
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Note: This sequence does not appear in the specification but has created from the wild type sequence (ABK13501) using information
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                                                                             AspValArgProIlePheTrpAlaAsnArgProLysSerTyrIleSerArgThrIleGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SerAspTyrGln-----PheMetArgProArgAlaArgAspLysLysLeuValGluGlu
                                                             TGGGACGAGTTCCCTAACGGCCGCTGGGGCAATTCCTCTTCCCCTGCCTTTGGGGAGCTG
                                                                                                                          GATGTACGTCCCATCTTCTGGGCCTCCAGACCAAAGAGTTACATCTACCGTACCCAGGAG
                                                                                                                                                                                        GACCCC----AGGCGTCCCCTACCCTGGGCTCTCAGTGCCCCAACCCCCAAGCGCCGAGAGGAA
                                                                                                                                                                                                                                                                                  ThrLeuAsnMetGluLysSerAlaLeuAlaIleLeuMetAsnLeuGlyLeuIleGluGlu
                                                                                                                                                                                                                                                                                                                                  GlyThrGluMetCysLysLysIleLeuAlaHisGly---IleLysThrLeuHisLeuTyr
                                                                                                                                                                                                                                                                                                                                                                            GACGTGATTGAGCCAATCAAAGACAACGATGCTGCCATCCGCAACTATGGCATCGAGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCCGATTTCATCACGCAGCTTTTCTTTGAGGCTGACACATTCTTCCGCTTTGTGAAG
                                                                                                                                                                                                                     SerLysValSerArgSerLeuProTrpArgArgProAlaAsnValPheArgValLysGlu
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                                                                                                                                                                                                                                                                                                                                           anticonvulsant; cerebroprotective; amyotrophic lateral sclerosis; anxiety; dementia; depression; epilepsy; Huntington's disease; migraine; demyelinating disease; multiple sclerosis; pain; Parkinson's disease; psychosis; stroke; cardiovascular disorder; cancer; osteoporosis; metabolic disease; endocrine disease; inborn error of metabolism; inflammation; immune disorder; human;
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                                                                                                                                                                                                                                                                                         colorectal carcinoma; neoplastic disease; renal disease;
1.5.1.20; mutant.
/product= "MTHFR"
/note= "Methylenetetrahydrofolate reductase"
replace(482,G)
                                                                                     /*tag=
                                                                                                                                                 Location/Qualifiers
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alcohol or drug intoxication, postinfection psychosis, postpartum psychosis, senile psychosis, traumatic psychosis and acute idiopathic psychotic illnesses. A new pharmaceutical composition is used for treating amyotrophic lateral sclerosis, anxiety, dementia, depression, epilepsy, Huntington's disease, migraine, demyelinating disease, multiple sclerosis, pain, Parkinson's disease, schizophrenia, psychoses, or stroke. Deficiency may be associated with diseases including cardiovascular disorders, cancer (e.g. neuroblastoma and colorectal carcinoma), osteoporosis, metabolic or endocrine disease, inborn errors of metabolism, inflammation, immune disorders, neoplastic disease and renal disease. This sequence encodes a mutant human methylenetetrahydrofolate reductase (MTHFR, EC number 1.5.1.20), in which however the product of the incention of metabolism, inflammation, metabolism, and of the incention of metabolism, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, inflammation, i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or a risk for or propensity to psychosis in a subject comprising determining the presence of a heterozygous methylenetetrahydrofolate reductase (MTHFR) mutant allele in a nucleic acid sample obtained from subject. The method is useful for diagnosing subjects at risk of, or suffering from a psychosis, particularly schizophrenia but includes manic-depressive disease, organic psychotic disorders, psychosis in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Diagnosing subjects at risk for or suffering from a psychosis, particularly schizophrenia comprises determining the presence o heterozygous methylenetetrahydrofolate reductase mutant allele subject
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; Page -; 102pp;
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P-PSDB; AAU75422.
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                                                             in claim 4 of the invention.
                                                                                                                                                   the method of the invention.
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      Pred. No.:
      5.19e-91
      Length:
      2220

      Score:
      979.00
      Matches:
      188

      Percent Similarity:
      63.72%
      Conservative:
      79

      Best Local Similarity:
      44.87%
      Mismatches:
      138

      Query Match:
      44.76%
      Indels:
      14

      DB:
      24
      Gaps:
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Alignment Scores:

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                                         41 TyrLysGlyPheIleArgMetThrGlyPheCysLysThrLysIleProAlaAspIleMet 60
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                                                                                                                                                                                                AlaArgValIleValThrGlnLeuPheTyrAspThrAspIlePheLeuLysPheValAsn
                                                                                     GCATGCACCGACATGGGCATCACTTGCCCCATCGTCCCCGGGATCTTTCCCCATCCAGGGC
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                                                                                                                               GAGGAGGAGTCCCCGCCCCCCACCATCATCCAGTACATCCACGACAACTACTTCCTGGTC
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                                        AACCTGGTGGACAATGACTTCCCACTGGACAACTGCCTCTGGCAGGTGGTGGAAGAC
                                                                                SerLeuValAspAsnAspTyr---IleAsnGlyAspLeuPheAlaValPheAlaAsp
                                                                                                                                                                    ProGluAspGluAlaSerArgLysLeuValGluGluValGlyGlySerHisPheLeuVal
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                                                                                                                                                                                                                                                                         P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  mutation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neuroblastoma; colorectal carcinoma; neoplastic disease; renal disease;
ss; EC number 1.5.1.20; mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Methylenetetrahydrofolate reductase; MTHFR; neuroleptic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human methylenetetrahydrofolate reductase (MTHFR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABK13541 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                        2002-130741/17.
)B; AAU75423.
                                                                                                                                                                                                                                                                                                                                           2000US-0592595
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                                                                                                                                                                                                                                                                                                                                                                                                                       /product= "MTHFR"
/note= "Methylenetetrahydrofolate
replace(559,C)
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag=
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Diagnosing subjects at risk for or suffering from a psychosis, particularly schizophrenia comprises determining the presence of particularly schizophrenia comprises determining the presence of particularly schizophrenia comprises. in a

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Page .: English

suffering from a psychosis, particularly schizophrenia but includes manic-depressive disease, organic psychotic disorders, psychosis in alcohol or drug intoxication, postinfection psychosis, postpartum psychosis, senile psychosis, traumatic psychosis and acute idiopathic psychotic illnesses. A new pharmaceutical composition is used for treating amyotrophic lateral sclerosis, anxiety, dementia, depression, epilepsy, Huntington's disease, migraine, demyelinating disease, multisclerosis, pain, Parkinson's disease, schizophrenia, psychoses, or stroke. Deficiency may be associated with diseases including The invention describes a method of diagnosing a psychosis in a subject, or a risk for or propensity to psychosis in a subject comprising determining the presence of a heterozygous methylenetetrahydrofolate reductase (MTHFR) mutant allele in a nucleic acid sample obtained from a subject. The method is useful for diagnosing subjects at risk of, or suffering from a maychosic particularly schizobers but includes methylenetetrahydrofolate reductase (MTHFR, EC number 1.5.1. nucleotide 559 has been altered to produce a mutant allele, of metabolism, inflammation, immune disorders, renal disease. This sequence encodes a mutant cardiovascular disorders, cancer (e.g. neuroblastoma and colorectal carcinoma), osteoporosis, metabolic or endocrine disease, inborn error for metabolism, inflammation, immune disorders, neoplastic disease arenal disease. This sequence encodes a mutant human described ĺn multiple

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Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the method of the invention. Note: This sequence does not appear in the specification but has created from the wild type sequence (ABK13501) using information in claim 4 of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2220 BP; 501 A; 657
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CTCACCATCAACTCACAGCCCAACATCAACGGGAAGCCGTCCTCCGACCCCATCGTGGGC
                                                                                                                                                                                                                                                                                  TGGGGGGAGGAGCTGACCAGTGAAGCAAGTGTCTTTGAAGTCTTTGTTCTTTACCTCTCG 1332
                                                                                                                                                        TrpAlaValProLeuLysSerValGluAspIleTyrGluArgPheArgLeuTyrCysLeu
                                                                                                                                                                                       AAGGACTACTACCTCTTCTACCTGAAGAGCAAGTCCCCCAAGGAGGAGCTGCTGAAGATG 1272
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                                             CTGGCGGCTGAGACCAGCCTGCTGAAGGAGGAGCTGCTGCGGGGTGAACCGCCAGGGCATC
                                                           LeuGlnProGluThrLysIleIleAsnGluGlnLeuGluLysIleAsnThrLysGlyPhe
                                                                                                                                                                                                             SerAspTyrGln-----PheMetArgProArgAlaArgAspLysLysLeuValGluGlu 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GACGTGATTGAGCCAATCAAAGACAACGATGCTGCCATCCGCAACTATGGCATCGAGCTG
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               GAGGAGGAGTCCCCGTCCCGCACCATCATCCAGTACATCCACGACAACTACTTCCTGGTC 1869
                                                                           ProGluAspGluAlaSerArgLysLeuValGluGluValGlyGlySerHisPheLeuVal 389
                                                                                                      TTCATGTTCTGGAAGGACGAGGCCTTTGCCCTGTGGATTGAGCGGTGGGGAAAGCTGTAT 1809
                                                                                                                          PheAsnValTrpLysAspGluAlaPheGluIleTrpSerArgGlyTrpAlaSerLeuTyr 369
                                                                                                                                                          GluLysLeuAspAlaLeuValAspLysCysLysAsp---ArgThrSerLeuThrTyrMet 309
                                                                                                                                                                                                                                                                                                                        ThrTrpGlyValPheProAlaLysGluIleIleGlnProThrIleValAspProValSer
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                                                                                                                                                                                                                                        AlaValAsnLysAspGlySerTrpLysSerAsnValGlyGlnThrAspValAsnAlaVal 329
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Search completed: February Job time: 301 secs 14, 2003, 23:16:00

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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 14, 2003, 21:20:31; Search time 41 Seconds (without alignments) 956.655 Million cell updates/sec

Title: Perfect score: Sequence: US-09-720-451-6 2187 1 ARVIVTQLFYDTD:

ARVIVTQLFYDTDIFLKFVN.....VSLVDNDYINGDLFAVFADF 408

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB : Maximum DB :

seq length: 0
seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 1008 Listing first 45 summaries

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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hypothetical prote	5,10-methylenetetr	5,10-methylenetetr	5,10-methylenetetr	5,10-methylenetetr	5,10-methylenetetr	5,10-methylenetetr	probable 5,10-meth	5,10-methylenetetr		5,10 methylenetetr	5,10-methylenetetr	methylenetetrahydr	5,10-methylenetetr	methylenetetrahydr	methvlenetetrahvdr	hypothetical prote	methylenetetrahydr	methylenetetrahydr	methvlenetetrahvdr	probable methylene	Description									

Query Match 83.9% Best Local Similarity 82.1% Matches 334; Conservative

83.9%; Score 1834; DB 2; 82.1%; Pred. No. 1.3e-138; ative 37; Mismatches 36;

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G85055	AG2534	AF2559	T27447	NNAHA	JQ0461	T10518	T28432	в70389	VHVNV4	C97080	S52835	в95068	C97936	AI3321
probable polyprote	nypothetical prote		hypothetical prote	nucleoprotein - ve	genome polyprotein	fruit bromelain (E	variant-specific s	translation elonga	nucleoprotein - ve		hypothetical prote	hypothetical prote	5,10-methylenetetr	5,10-methylenetetr

## ALIGNMENTS

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A; Accession: T47821
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-592 < DNA
A; Residues: 1-592 < DNA
A; Cross-references: EMBL: ALL38647
A; Cross-references: EMBC: ALL38647
C; Genetics:
A; Map position: 3
A; Introns: 155/1; 182/3; 240/3; 298/3; 332/2
A; Note: F24G16.240
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747821
methylenetetrahydrofolate reductase MTHFR1 - Arabidopsis thaliana
methylenetetrahydrofolate reductase MTHFR1 - Arabidopsis thaliana
methylenetes: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr:2000 #sequence_revision 20-Apr:2000 #text_change 20-Apr:2000
C;Accession: T47821
R;D'Angelo, M: Vezzi, A: Modesto, D: Pigazzi, M: Valle, G: Mewes, H.W.:
submitted to the Protein Sequence Database, February 2000
A;Reference number: Z24477
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C;Species: Schizosaccharomyces pombe
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                                                                                                                             WSRGWASLYPEDEASRKLYEEVGGSHFLYSLYDNDYINGDLFAVFA 406
                                                                                                                                                                                           KDRTSLTYMAVNKDGSWKSNVGQTDVNAVTWGVFPAKEIIQPTIVDPVSFNVWKDEAFEI
                                                                                                                                                                                                                                                                      QLEKINTKGFLTINSQPAVNGEKSDSPTVGWGGPGGYVYQKAYVEFFCSKEKLDALVDKC
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                                                                                                                                                                                                                                                                                                                                                                                                                             AALEPIKDNDEAVKAYGIHFATEMCKKILAHGITSLHLYTLNVDKSAIGILMNLGLIDES
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   #text_change
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                                   (Schizosaccharomyces
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A;Map po
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   A;Molecule type: DNA
A;Residues: I-113,'KRRSS' <HOS>
A;Cross-references: EMBL:D21200
R;Kitakawa, M.; Graack, H.R.; G;
Eur. J. Biochem. 245, 449-456,
                                                                                                 A; Reference number: JX0365; A; Accession: S53294
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                                                                                 A; Status: translation not
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C;Accession: T38920
R;Pearson, D.; Churcher, C.M.; Barrell, B.G.; Rajandream, submitted to the EMBL Data Library, February 1996
A;Reference number: Z21817
A;Accession: T38920
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: strain C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:Z69728; PID A;Experimental source: strain 972h-;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-603 < PEA>
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Best Local
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528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     ARVIVTQLFYDTDIFLKEVNDCRQIGITCPIVPGIMPINNYKGEIRMTGECKTKIPADIM
                                                                                                                                                                                                                                                                                                            KVSRSLPWRRPANV-----FRVKEDVRPIFWANRPKSYISRTIGWDQYPHGRWGDS
                                                                                                                                                                                                                                                                                                                                                          AALEPIKDNEEAVKAYGIHLGTEMCKKILAHGIKTLHLYTLNMEKSALAILMNLGLIEES
                                                                                                                                                                                                                RSPAFGEFDAIRYGLRMSP----KEITTSWGSP-KSYSEIGDLFARYCEKKISSLPWSDL
                                                                                                                                                                                                                                                                                                                                                                                                                              ADFIVTQMFYDVDNFIAWVDKVRAAGINIPIFPGIMPIQAWDSFIRRAKWSGVKIPQHFM
                                                                                                                                                                                                                                    CNPSYGALSDYQF----MRPRARDKKLVEEWAVPLKSVEDIYERFRLYCLGKLRSNPWSEL
SFLAWKDEAYSL-GMEWANAYSPDSISRKLLVSMMKEWFLCVIVDNDFQNGQSLFDVF
                  SFNVWKDEAFEIWSRGWASLYPEDEASRKLVEEVGGSHFLVSLVDNDYING-DLFAVE 405
                                                                      HPSLLNELKETVKKLNSVSYFVTNKNGDLDTNSQYEIPNAVTWGVFPNREIIQPTIVEST
                                                                                        SKEKLDALVDKCKDRTSLTYMAVNKDGSWKSNVGQTDVNAVTWGVFPAKEIIQPTIVDPV
                                                                                                                                        P-ISDEADLIRDQLLSMNRNAFLTINSQPALNGEKSSHPVFGWGPPNGYVFQKPYVEFFV
                                                                                                                                                                          DGLQPETKIINEQLEKINTKGFLTINSQPAVNGEKSDSPTVGWGGPGGYVYQKAYVEFFC
                                                                                                                                                                                                                                                                                    LA----PIVDTNNVELTNASSQDRRINEGVRPIFWRTRNESYVSRTDQWDELPHGRWGDS
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2h-; cosmid c56F8
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Pred. No. 1.
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.6e-63;
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methylenetetrahydrofolate reductase (NADPH2) (EC 1.5.1.20) MET13 - yeast (S. N.; Alternate names: protein G2882; protein YGL125w; ribosomal protein YML45, CSpecies: Saccharomyces cerevisiae C; Species: Saccharomyces cerevisiae C; Date: 17-May-1996 #sequence\_revision 17-May-1996 #sequence\_revision 17-May-1996 #sequence\_revision 17-May-1996 #text\_change 03-Jun-2002 C; Accession: S64136; S53294; S78029; S72026 R; Cerdan, E.; Rodriguez-Torres, A.M.; Rodriguez-Belmonte, E.; Tizon, B.; Cav. R; Cerdan, E.; Rodriguez-Torres, A.M.; Rodriguez-Belmonte, E.; Tizon, B.; Cav. R; Cerdan, E.; Rodriguez-Torres, A.M.; Rodriguez-Belmonte, E.; Tizon, B.; Cav. R; Cerdan, E.; Rodriguez-Torres, A.M.; Rodriguez-Belmonte, E.; Tizon, B.; Cav. R; Cerdan, E.; Rodriguez-Torres, A.M.; Rodriguez-Belmonte, E.; Tizon, B.; Cav. R; Cerdan, E.; Rodriguez-Torres, A.M.; Rodriguez-Belmonte, E.; Tizon, B.; Cav. R; Cerdan, E.; Rodriguez-Torres, A.M.; Rodriguez-Belmonte, E.; Tizon, B.; Cav. R; Cerdan, E.; Rodriguez-Torres, A.M.; Rodriguez-Belmonte, E.; Tizon, B.; Cav. R; Cerdan, E.; Rodriguez-Torres, A.M.; Rodriguez-Belmonte, E.; Tizon, B.; Cav. R; Cerdan, E.; Rodriguez-Torres, A.M.; Rodriguez-Belmonte, E.; Tizon, B.; Cav. R; Cerdan, E.; Rodriguez-Torres, A.M.; Rodriguez-Belmonte, E.; Tizon, B.; Cav. R; Cerdan, E.; Cav. R; Cerdan, E.; Cav. R; Cerdan, E.; Cav. R; Cerdan, E.; Cerdan, E.; Cerdan, E.; Cerdan, E.; Cerdan, E.; Cerdan, E.; Cerdan, E.; Cerdan, E.; Cerdan, E.; Cerdan R;Hosaka, K.; Nikawa, J.; Kodaki, T.; Ishizu, H.; Yamashita, J. Biochem. 116, 1317-1321, 1994
A;Title: Cloning and sequence of the SCS3 gene which is requ A; Cross-references: EMBL: 272647; NI A; Experimental source: strain S288C A; Molecule type: DNA A; Reference number: S64134 A; Accession: S64136 R;Cerdan, E.; Rodriguez-Torres, A.M.; Rodriguez-Belmonte, submitted to the Protein Sequence Database, May 1996 A; Residues: 1-599 < CER> ce of the SCS3 gene which is MUID:95221330; PMID:7706223 NID:g1322686; PIDN:CAA96833.1; required တ PID:g1322687; for yeast (Saccharomyc ln YmL45, mitochond inositol Cadahia, prototr

shown

Grohmann, 1997

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Goldschmidt-Reisin,

s.;

Herfurth,

(F)

Wit

from GB/EMBL/DDBJ

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RESULT 5
T15423
hypothetical protein C06A8.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #t.
C;Accession: T15423
R;Leimbach, D.
submitted to the EMBL Data Library, November 1995
n.Description: The sequence of C. elegans cosmid C06?
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A:Residues: 39-40,'LA',43-47,'A',49 <KIT>
A:Residues: 39-40,'LA',43-47,'A',49 <KIT>
A:Residues: 39-40,'LA',43-47,'A',49 <KIT>
A:Rote: this protein was identified as ribosomal protein YmL45, mitochondrial R:Tizon, B.; Rodriguez-Torres, A.M.; Rodriguez-Belmonte, E.; Cadahia, J.L.; C'yeast 12, 1047-1051, 1996
A:Title: Identification of a putative methylenetetrahydrofolate reductase by A:Reference number: S72026; MUID:97051592; PMID:8896269
A:Accession: S72026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Function: <METH>
A; Description: oxidoreductase
A; Note: this function seems to
C; Function: <RIB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Pathway: protein biosynthesis
A; Note: this function seems to contradict of C; Keywords: mitochondrion; oxidoreductase;
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A;Cross-references: MIPS:YGL125w;
A;Map position: 7L
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A; Residues: 1-72, 'R', 74-599 <TIZ>
A; Cross references: EMBL: X94106; NID: 91628448; I
A; Note: this protein was identified as putative
A;Description: The sequence of A;Reference number: Z18348 A;Accession: T15423
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LAWKEEFYHILNEWKLNMNKYDKPHSAQFIQSLIDDYCLVNIVDNDYISPD
                                                                                                                                                                                                                      NVWKDEAFEIWSRGWASLYPEDEA-SRKLVEEVGGSHFLVSLVDNDYINGD
                                                                                                                                                                                                                                                                                  KLDALVDKCKDRTSLTYMAVNKDGSWKSN-VGQTDVNAVTWGVFPAKEIIQPTIVDPVSF
                                                                                                                                                                                                                                                                                                                                               QPETKIINEQLEKINTKGFLTINSQPAVNGEKSDSPTVGWGGPGGYVYQKAYVEFFCSKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IITQMFYDVDNLLNWCSQVRAAGMDVPIIPGIMPITTYAAFLRRIQWGQISIPQHFSSRL
                                                                                                                                                                                                                                                                KLPKLIDTLKNNEFLTYFAIDSQGDLLSNHPDNSKSNAVTWGIFPGREILQPTIVEKISF
                                                                                                                                                                                                                                                                                                                           NDEINPIKAHLIELNQHSIITINSQPQVNGIRSNDKIHGWGPKDGYVYQKQYLEFMLPKT
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Pred. No. 3.5e-54;
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                                C06A8
                                                                                         #text_change
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piosynthesis; ribosome
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A;Molecule type: I
A;Residues; 1-615
A;Cross-reference:
C;Genetics:
A;Gene: CESP:C06A!
A;Introns: 28/2;
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A; Residues: 1-641 < MUR>
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                                                                                                                                                                                                                                                                               A; Cross-references:
                                                                                                                                                                                                                                                                                                                                        A; Accession: T38659
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                                                                                                                                                                                                                                Genetics:
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:Introns: 28/2; 53/2;
                                                                                                                                                       Matches
                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                  position:
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158; Conservative
                                                                                                                                                      Conservative
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                                                                                                                                                                     28.8%;
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methylenetetrahydrofolate reductase 2 - fission yeast (Schizosaccharomyces c;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 20-Jun-2000 C;Accession: T38659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; Murphy, L.; Harris, D.; Wood, V.; submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cross-references: EMBL:U39849; NID:g1055041; PID:g1055045; PIDN:AAA81048.1; CESP:C0
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                                                                                         ADIMAALEPIKDNEEAVKAYGIHLGTEMCKKIL-----AHGIKTLHLYTLNMEKSALAI 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DPLSFRAWRDEAYQMWMAQWGDFYPKESKSYGVIKAVHDEFRLVTLVDNDF
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                                                  SSLMQRLNAAKPDDEAIKNIGVEHIVDMIKKIMDNVQGRVHG---FHFCTLNLERSVALI
                                                                                                                                                       ADFIITQIFYEPEAFIKFENFVRNHSSNALRNIPIIPAIMPIQSYGSLKRMTRLCGCSVP 243
                                                                                                                                                                                                    ARVIVTQLFYDTDIFLKFVNDCRQIGITC----PIVPGIMPINNYKGFIRMTGFCKTKIP
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EESKVSRS-
                                                                                                                                                                                                                                                    ; Score 629; DB 2;
; Pred. No. 3.2e-42;
80; Mismatches 161
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August 1997
                                                                                                                                                                                                                                                         161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSPDB:GN00066;
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  LPWRRP----ANVFR 136
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RESULT 7
$63459
methylenetetrahydrofolate reductase (NADPH2) (EC 1.5.1.20) MET12 - yeast (Saccharomyces methylenetetrahydrofolate reductase (NADPH2) (EC 1.5.1.20) MET12 - yeast (Saccharomyces N;Alternate names: protein LPB8c; protein YPL023c
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Apate: 16-May-1996 #sequence_revision 12-Jul-1996 #text_change 03-Jun-2002
C;Accession: S63459
C;Accession: S63459
A;Reference number: S63452
A;Accession: S63459
A;Accession: S63459
A;Accession: S63459
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A;Cross-references: SGD:S0005944; MIPS:YPL023c
A;Map postition: 16L
C;Keywords: oxidoreductase
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A;Residues: 1-657 <WANN
A;Cross_references: EMBL:U36624; NID:g1276642; PIDN:AAB68164.1; PID:g1039454; GSPDB:GN0
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           EFFCSKEKLDALVDKCKD---RTSLTYMAVNKDGSWKSNVGQTDVNAVTWGVFPAKEIIQ 341
                                          WSDL-GLSAETALIQEELIQLNYRGYLTLASQPATNATLSSDK1FGWGPAKGRLYQKAFV
                                                                     WSELDGLQPETKIINEQLEKINTKGFLTINSQPAVNGEKSDSPTVGWGGPGGYVYQKAYV 284
                                                                                                     REGDSRSPAYGEIDGY---GPSIKVSKSKALELWGIP-KTIGDLKDIFIKYLEGSTDAIP
                                                                                                                      FRVKEDVRPIFWANR-------PKSYIS-----RTIGWDQYPHG 166
                                                                                                                                                                                                                                VLSHIVNESSEEGEDETSGEIGSIENVPIEDADGDIVLDDSNEETVANRKR--RRHSSL
                                                                                                                                                                                                                                                                                           LSRFPPEIQSDDNAVKSIGVDILIELIQEIYQRTSGRIKGFHFYTLNLEKAIAQIVSQSP
                                                                                                                                                                                                                                                                                                                      MAALEP-IKDNEEAVKAYGIHLGTEMCKKI---LAHGIKTLHLYTLNMEKSALAILM~-- 112
                                                                                                                                                                                                                                                                                                                                                        ADFVITQLFYDVEKFLTFEMLFRERISQDLPLFPGLMPINSYLLFHRAAKLSHASIPPAI 242
                                                                                                                                                                                                                                                                                                                                                                          ARVIVTQLFYDTDIFLKFVNDCRQ-IGITCPIVPGIMPINNYKGFIRMTGFCKTKIPADI
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                                                                                                                                                                   ----DSAKLIF---NRAIVTEKGLRYNNENGSMPSKKALISISKGHGTLGRDATWDEFPNG
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                                                                                                                                                  Similarity
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RESULT 8
$46454

Nature Genet. 7, 195-200, 1954

Nature Genet. 7, 195-200, 1954

A;Title: Human methylenetetrahydrofolate reductase (FADH2) (EC 1.7.99.5) - human

C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Accession: $46454

Nature Genet. 7, 195-200, 1994

Nature Genet. 7, 195-200, 1994

A;Title: Human methylenetetrahydrofolate reductase: isolation of cDNA, mapping and mu

A;Reference number: $46454

A;Accession: $46454

A;Accession: $46454

A;Accession: $46454

A;Accession: $46454

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A;Accession: $46454

A;Accession: $46454

A;Accession: $46454
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C; Keywords: FAD; oxidoreductase
                                                                                                                                                                                                                                                                   ARVIVTQLFYDTDIFLKFVNDCRQIGITCPIVPGIMPINNYKGFIRMTGFCKTKIPADIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTIVDPVSENVWKDBAFEIWSROWASIKPEDBASRKLYEEVGGSHFLVSLVDNDINGD 400
                                                                                                                                                               SKVSRSLPWRRPANVFRVKEDVRPIFWANRPKSYISRTIGWDQYPHGRWGDSCNPSYGAL
                                                                                                                                                                                                                                      DVIEPIKDNDAAIRNYGIELAVSLCQELLASGLVPGLHFYTLNREMATTEVLKRLGMWTE
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                                                          SDYOFMRPRARDKK 193
                                                                                                                    DP-RRPLPWALSAHPKRREEDVRPIFWASRPKSYIYRTQEWDEFPNGRWGNSSSPAFGEL
                                                                                                                                                                                                                                                                                                                                                    ADFIITQLFFEADTFFRFVKACTDMGITCPIVPGIFPIQGYHSLRQLVKLSKLEVPQEIK 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 486; DB 2;
Pred. No. 4.7e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67;
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                                                                                                                        401
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methylenetetrahydrofolate reductase homolog - fission yeast (Schizosaccharomyces C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 21-Jul-2000 C;Accession: T42227 R;YOShioka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.
DNA Res. 4, 363-369, 1997
A;Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.
A;Reference number: Z17323; MUID:98162722; PMID:9501991
A;Accession: T42227 A;Cross-references: EMBL:D89118; NID:g1749443; PIDN:BAA13780.1; A;Experimental source: strain PR745 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-566 <YOS> 234 SSLMQRLNAAKPDDEAIKNIGVEHIVDMIKKIMDNVQARVHG---FHFCTLNLERSVALI 290 ADIMAALEPIKDNEEAVKAYGIHLGTEMCKKIL ----- AHGIKTLHLYTLNMEKSALAI 110 ADFIITQIFYEPEAFIKFDNFVRNHSSNALRNIPIIPAIMPIQSYGSLKRMTRLCGCSVP Conservative 19.3%; 56; Score 421.5; DE Pred. No. 1e-25; Mismatches DB 2; 127; Indels Length 67; PID: g1749444 Gaps 233 56 12; pomb

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A; Title: The complete genome of A; Reference number: A70300; MUJ A; Reference number: A70424
A; Status: preliminary; nucleic A; Molecule type: DNA
A; Residues: 1-296 <AQF>
A; Cross references: GB: AE000740
A; Experimental source: strain V C; Gene: metf
C; Superfamily: 5,10-methylenete
                                                                                                                                                                                                                                             RESULT 11
D70424
5,10-methylenetetrahydrofolate reductase - Aquifex aeolicus
5,10-methylenetetrahydrofolate reductase - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Species: 08-May-1998 #sequence_revision 08-May-1998 #text_change 11-Jun-1999
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 11-Jun-1999
C;Accession: D70424
C;Accession: D70424
C;Accession: D70424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AE004480; GB:AE004091; A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-290 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Complete genome sequence of Pseudomonas aeruginosa A;Reference number: A82950; MUID:20437337; PMID:10984043 A;Accession: F83591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Stover, C.K.; Pham, X.Q.; adman, S.; Yuan, Y.; Brody, .; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision
C;Accession: F83591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5,10-methylenetetrahydrofolate reductase PA0430 [imported] -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
                                                                                                                                                                                                            Nature 392, 353-358, 1998
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                              237 AYGDDSRSIQAFGEQVISEMCERLLEGGAPGLHFYTLNQADPSLAIWKNLQL 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          metF; PA0430
                                                                                                                                                                                                                                                                                                                                                                                                                                           PIKDNEEAVKAYGIHLGTEMCKKILAHGIKTLHLYTLNMEKSALAILMNLGL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ITQYFFNADAYFYFVERVAKLGVDIPVVPGIMPITNYSKLARFSDACGAELPRWIRKQLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LKNSGLLTKRWKQVESEMEDEKLLRTTRKRLSLDEPAELHNQVVVPSQQPVADKSSNLFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LMNLGLI----
                                                                                                                              preliminary; nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LKLNGNSWWTVGSQPAVNGAPSADPVFGWGPKGGRVFQKAFVECFVNGKDLKDFITKWHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EKINTKGFLTINSQPAVNGEKSDSPTVGWGGPGGYVYQKAYVEFFCSKEKLDALVDKCKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TLHEPPSEALKL -- - WGYPVDE - SDITSLEQKHIMSDISVIPWID - EPVEVETKTIAKYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QFMRPRARDKKLVEEWAVPLKSVEDIYERFRLYCLGKLRSNPWSELDGLQPETKIINEQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TSKQSSVSGHKDNLTEEAP-FSVSEGSGVLGRQANWDDFTNGRFGDPRSPAYGEIDGYGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
    5,10-methylenetetrahydrofolate
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                                                           GB:AE000740; NID:g2983826; ce: strain VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -DVRPIFWANRPKSYISRTIGWDQYPHGRWGDSCNPSYGALSDY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Erwin,
L.L.; (
                                                                                                                                                                       e of the hyperthermophilic bacterium MUID:98196666; PMID:9537320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 222;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Coulter, S.N.; Folger,
                                                                                                                                    sequence not shown;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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      reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NID: g9946284;
                                                                           PIDN: AAC07387.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 290
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                                                                                                                                    translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Warrener,
K.R.; Kas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIDN: AAG03819.1;
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                                                                                                                                                                                        Aquifex aeolicus
                                                                             PID:g2983832;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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Larbig,
                                                                                                                                                                                                                                               Graham,
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                                                                             GB: AE00065
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K.; Lim,
                                                                                                                                                                                                                                               D.E.;
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A;Cross-references: (C;Genetics: A;Gene: CC2140 C;Superfamily: 5,10-n
                                                                                                                                                                                                                                                                                                                                                C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001 C;Accession: C87514
C;Accession: C87514
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko n. J.; Ermolaeva, M.; White, O; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C proc. Natl. Acad. Sci. U.S.A. 9436-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; pMID:11259647
                                                                                                                                                                                                                                                                  A;Reference number: A87249;
A;Accession: C87514
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-314 <STO>
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;Species: Caulobacter crescentus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                            Query Match
Best Local
                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178
191 ISQFFFDLDAFLFFVDKVRAAGITIFIVPGIMPVTNFAGLKKMAAACQTAIPSWLGNLFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      238 KVEDKPEEVKKIGIEFAINQCLDLIEHGVPGLHFYTLNKSDATLKI 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 VTQLFYDTDIFLKFVNDCRQIGITCFIVPGIMPINNYKGFIRMTGFCKTKIPADIMAALE 64 :||:|: | : : !|
                                             σ
                          PIKDNEEAVKAYGIHLGTEMCKKILAHGIKTLHLYTLNMEKSALAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ITQMFFVNDYYYRFVEMCKNAGIDISIIPGIMPITNFKQIRKFASLCGATIPQSLIEKLE 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l Similarity
40; Conser
                                                                                                               Similarity
                                                                                                                                                                           5,10-methylenetetrahydrofolate reductase (FADH2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                           Conservative
                                                                                                                                                                                                                                             GB:AE005673; NID:g13423631;
                                                                                         10.1%; Score 221; DB 2; 137.9%; Pred. No. 4.9e-10; 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 222; DB 2;
Pred. No. 3.8e-10;
7; Mismatches 49
                                                                                                                                                                                                                                               PIDN: AAK24111.1;
                                                                                                                                Length 314;
                                                                                       Indels
                                                                                           0,
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                                                                                           Gaps
                                                64
                                                                                           0;
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251 GLENDAETRRLIACSVAAEMCAKLQEQGFEDFHFYTLNRADLVYAICRVLGVREIS 65 PIKDNEEAVKAYGIHLGTEMCKKILAHGIKTLHLYTLNMEKSALAILMNLGLIEES

250

5,10-methylenetetrahydrofolate reductase XF1121 [imported] - Xylella f C;Species: Xylella fastidiosa C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Sep C;Accession: F82720 R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nature 406, 151-157, 2000 A;Title: The genome sequence of the plant pathogen Xylella fastidiosa. A;Reference number: A82515; MUID:20565711; PMID:10910347 A;Note: for a complete list of authors see reference number A59328 bel A;Accession: F82720 A;Cross-references: GB:AE003948; GB:AE003849; NID:g9106078; PIDN:AAF83931.1; GSPDB:GN
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marxino, C.L.; Marques, M.V.; Martins
a;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C A; Molecule type: DNA A; Residues: 1-275 <SIM> A; Status: preliminary #text\_change 02-sep-2000 Xylella fastidiosa for Nucleotide (stra

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R;Saunders, D.C.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, submitted to the EMBL Data Library, August 1999
A;Reference number: Z21563
A;Accession: T34973
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Experimental source: strain A3(2)
C;Genetics: A;Gene: metF; SCOEDB:SC4A10.36c
C;Superfamily: 5,10-methylenetetrahydrofolate reductase (FADH2)
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C; Species;
C; Date: 05
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                                             RESULT 15
H64123
C;Species: Haemophilus influenzae
C;Species: Haemophilus influenzae
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C;Species: Haemophilus influenzae
C;Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: H64123
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, &
Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman,
Gocayne, J.D., Scott, J.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
P.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
P.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fritchman, J.L.; Geoghagen, N.S.M.
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
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Cross references: GB:U32823; GB:L42023; NID:g1574281; PIDN:AAC23094.1; PID:g1574284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .10-methylenetetrahydrofolate reductase (FADH2) (EC 1.7.99.5) - Haemophilus influenzae Speciles: Haemophilus influenzae Speciles: Haemophilus influenzae Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 Accession: H64123
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Superfamily: 5,10-methylenetetrahydrofolate reductase (FADH2)
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Saunders, D.C.; Ha
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l Similarity 33.9%;
39; Conservative 3
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C; Superfamily: 5,10-methylenetetrahydrofolate reductase (FADH2) C; Keywords: methionine biosynthesis; oxidoreductase
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Query Match
8.6%; Score 189; DB 1; Length 292;
Best Local Similarity 32.8%; Pred. No. 1.6e-07;
Matches 38; Conservative 23; Mismatches 55; Indels 0; Gaps
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14-JUL-1999; Glycine max. (DUPO ) DU PONT DE NEMOURS & CO 15-JUL-1998; 27-JAN-2000. WO200004163-A1 98US-0092869 99WO-US15916 sequence"
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RESULT 2
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                  Arabidopsis thaliana
                                                                                                                  Arabidopsis thaliana protein fragment SEQ ID NO: 60184.
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sation assay; genetic mapping; gene expression control; promoter;
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                                                                                                                                                                                                 Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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> 99US-0145088. 99US-0145085. 99US-0145087. 99US-0145089.

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25-FEB-2000; 2000EP-0301439
                   06-SEP-2000.
                                    EP1033405-A2
                                                      Arabidopsis thaliana
                                                                                                             Arabidopsis thaliana protein fragment SEQ ID NO: 60182.
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162 ADLIVTQLFYDTDIFLKFVNDCRQIGISCPIVPGIMPINNYRGFLRMTGFCKTKIPVEVM
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Pred. No. 5.9e-175;
17; Mismatches 36;
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pathway;
promoter;

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          AAG32203 standard;
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                                                                  WSRGWASLYPEDEASRKLVEEVGGSHFLVSLVDNDYINGDLFAVFAD
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nilarity 82.1%;
Conservative 3
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37; Mismatches
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5.3e-175;
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hybridisation assay; genetic mapping; gene expression control;
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5.5e-175;
nes 36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana protein fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana
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|| 1||: || 1||||||:|| 456
|| QLGKINSNGFLTINSOPSVNAAKSDSPAIG 456
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netic mapping; gene expression control;
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promoter;
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12-AUG-1999;
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ADLIVTQLFYDTDIFLKFVNDCRQIGINCPIVPGIMPISNYKGFLRMAGFCKTKIPAELT 273
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99US-0151065
                                                    54.1%;
78.9%;
                                           28;
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Pred. No. 9.7e-110;
8; Mismatches 29;
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                                                             Length 497;
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RESULT 14
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                                                                                                          Query Match
Best Local S
Matches 188
                                                                                                                                                                                                                                              This is the protein sequence encoding human MTHFR, the gene of which has been localised to chromosome 1p36.3. Deficiencies of this protein may lead to cardiovascular and neurological disorders and disorders influences by folic acid metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Human methylene:tetra:hydro:folate reductase cDNA probe - for detection of sequence abnormalities in methylene:tetra:hydro:folate reductase e.g. in cardiovascular, neurological or folic acid
                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig.6A-6C; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Methylene-tetrahydrofolate-reductase; MTHFR; gene therapy; cardiovascular disease; neurological disease; folic acid metabolism; EC-1.5.1.20; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                              metabolism disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Goyette P,
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ADFITTQLFFEADTFFRFVKACTDMGITCPIVPGIFPIQGYHSLRQLVKLSKLEVPQEIK 281
                                 ARVIVTQLFYDTDIFLKFVNDCRQIGITCPIVPGIMPINNYKGFIRMTGFCKTKIPADIM 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1996-030565/03.
DB; AAT09689.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DYQFMRPRARDKKLVEEWAVPLKSVEDIYERFRLYCLGKLRSNPWSELDGLQPETKIINE
                                                                                                          188;
                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
                                                                                                                                                                                                       656 AA;
                                                                                                          Conservative
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44.9%;
                                                                                                       79;
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                                                                                             Score 979; DB 1/, Pred. No. 6e-89; ""smatches 138;
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                                                                                                                                                   Length 656;
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                                                                                                     14;
                                                                                                  Gaps
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61 AALEPIKDNEEAVKAYGIHLGTEMCKKILAHG-IKTLHLYTLNMEKSALAILMNLGLIEE 119

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ARESULT 15
ARE12607
ID ARE12
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                                                           5-methylenetetrahydrofolate, a co-substrate for methylation of homocysteine to methionine. The invention provides potential therapy for individuals with MTHFR deficiency. The non allele-specific antisense nucleic acids are useful for treating, stabilising or preventing cancer,
                                                                                                                                                                                                  The invention relates to a non allele-specific antisense nucleic acids, which binds to methylenetetrahydrofolate reductase (MTHFR; EC 1.5.1.20) which binds to methylenetetrahydrofolate reductase (MTHFR; EC 1.5.1.20) nucleic acids and inhibits MTHFR protein expression in a mammal. MTHFR catalyses the NADPH-linked reduction of 5,10-methylenetetrahydrofolate to
                                                                                                                                                                                                                                                                                                                                                                                                                                                               New antisense nucleic acids, which are methylenetetrahydrofolate reductase inhibitors, useful for treating, stabilizing or preventing cancer, e.g. breast carcinoma, colon carcinoma, colorectal carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US2001025030-A1
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   particularly breast carcinoma, colon carcinoma, colon particularly breast carcinoma, hancreatic cancer, kidney
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                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 6; 68pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                           neuroblastoma
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SEKHON J.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                               AALEPIKDNEEAVKAYGIHLGTEMCKKILAHG-IKTLHLYTLNMEKSALAILMNLGLIEE 119
                                                                                                                                        LQPETKIINEQLEKINTKGFLTINSQPAVNGEKSDSPTVGWGGPGGYVYQKAYVEFFCSK
                                                                                                                                                                       KDYYLFYLKSKSPKEELLKMWGEELTSEASVFEVFVLYLSGEPNRNGHKVTCLPWND-EP
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                         FNVWKDEAFEIWSRGWASLYPEDEASRKLVEEVGGSHFLVSLVDNDY-INGDLFAVFAD 407
                                                                                  EKLDALVDKCKD-RTSLTYMAVNKDGSWKSNVGQTDVNAVTWGVFPAKEIIQPTIVDPVS
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FMFWKDEAFALWIERWGKLYEEESPSRTIIQYIHDNYFLVNLVDNDFPLDNCLWQVVED
                                                        ETAEALLQVLKKYELRVNYHLVNVKGENITNAPELQPNAVTWGIFPGREIIQPTVVDPVS
                                                                                                              {\tt LAAETSLLKEELLRVNRQGILTINSQPNINGKPSSDPIVGWGPSGGYVFQKAYLEFFTSR}
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Pred. No. 6e-89;
9; Mismatches 1
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Search completed: February 14, Job time: 73 secs 2003, 23:07:42

GenCore version Copyright (c) 1993 - 2003 5.1.3 Compugen Ltd.

OM protein - protein search, using sw model

Run on : February 14, 2003, 19:26:12; Search time 22 Seconds

(without alignments)
769.197 Million cell updates/sec

Title: Perfect score: US-09-720-451-6 2187

ARVIVTQLFYDTDIFLKFVN.....VSLVDNDYINGDLFAVFADF 408

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum Maximum DB DB seq length: 0 seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

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RESULT 2
MTHR_HI
ID MTHR_HI
AC P42898
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MIlos R., Goyette
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gene and genotype/phenotype correlations in severe
methylenetetrahydrofolate reductase deficiency.";
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Matthews R.G., Rozen R.;
Matthews R.G., Rozen R.;
Genet. 7:551-551(1994).
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                                                                                                                                                                               reductase (MTHFR) MTHFR.";
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"Identification of four novel mutations methylenetetrahydrofolate reductase defi Eur. J. Hum. Genet. 6:257-265(1998).
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Weisberg I., Tran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANTS SER-324 AND GLY-339.
MEDLINE=98454315; PubMed=9781030;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              isberg I. Tran P., Christiensen B., second genetic polymorphism in methigraphs associated with decreased enzyn Genet. Metab. 64:169-172(1998).
                                                                                                                                                                                                                                                                                                                       s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBI outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way iffed and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                             POLYMORPHISM: VARIANT VAL-222 IS A COMMON POLYMORPHISM WHICH HAS BEEN INPLICATED IN THREE MULTIFACTORIAL DISEASES: OCCLUSIVE BEEN INVLICATED IN THREE MULTIFACTORIAL DISEASES: OCCLON CANCER. DISEASE: DEFECTS (IN MTHER ARE THE CAUSE OF HOMOCYSTEINEMIA (HOMOCYSTENINIA II), AN AUTOSOMAL RECESSIVE DISEASE WHICH SHOWS WIDE RANGE OF CLINICAL SYMPTOSOM, SUCH AS DEVELOPMENTAL DELAY, SEVERE MENTAL RETARDATION, PERINATAL DEATH, PSYCHIATRIC DISTURBANCES, AND LATER-ONSET NEURODEGENERATIVE DISORDERS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: CATALYZES THE CONVERSION OF 5.10-
METHYLEMETETRAHYDROFOLATE TO 5-METHYLITERAHYDROFOLATE,
SUBSTRATE FOR HOMOCYSTEINE REMETHYLATION TO METHIONINE.
CATALYTIC ACTIVITY: 5-methyltetrahydrofolate + NADP(+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: CATALYZES THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PATHWAY: Folate metabolism. SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            methylenetetrahydrofolate + NADPH. COFACTOR: FAD.
                                                     AF105978; AAD17965.1; J
AF105979; AAD17965.1; J
AF105980; AAD17965.1; J
AF105981; AAD17965.1; J
AF105982; AAD17965.1; J
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AF105983; AAD17965.1; J
AF105984; AAD17965.1; J
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AF105987; AAD17
AF105977; AAD17
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                                         HGNC: 7436;
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IPR004621; Fadh2_euk
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                                                                                                                                                                                                                        AAD17965.
AAD17965.
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deficiency.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                    Oxidoreductase; Flavoprotein; FAD; SEQUENCE 654 AA; 74649 MW; 12A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9WU20;
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                          TIGRFAMS;
                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR004621; Fadh2_euk.
InterPro; IPR003171; Mehydrof_redctse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rozen R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goyette P., Pai A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=98345426; PubMed=9680386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Last annotation update)
Methylenetetrahydrofolate reductase (EC 1.5.1.20)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel.
16-OCT-2001 (Rel.
16-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MTHR_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MTHFR
       221
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                                                                                                                                                                             Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENZYME REGULATION: ALLOSTERIČALLY REGULATED BY S-ADENOSYLMETHIONINE (BY SIMILARITY).

PATHWAY: FOLATE metabolism.

SUBUNIT: HOMODIMER (BY SIMILARITY).

SIMILARITY: BELONGS TO THE METHYLENETETRAHYDROFOLATE REDUCTASE (EC 1.5.1.20/EC 1.7.99.5) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                m. Genome 9:652-656(1998).

FUNCTION: CATALYZES THE CONVERSION OF 5,10-
METHYLENETETRAHYDROFOLATE, A METHYLENETETRAHYDROFOLATE, A SUBSTRATE FOR HOMOCYSTEINE REMETHYLATION TO METHIONINE.

CATALYTIC ACTIVITY: 5-methyltetrahydrofolate + NADP(+) = methylenetetrahydrofolate + NADPH.

COFACTOR: FAD (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGI:106639;
ADFIITQLFFEASTFFSFVKACTEIGISCPILPGIFPIQGYTSLRQLVKLSKLEVPQKIK 280
                                                              ARVIVTQLEYDTDIFLKEVNDCRQIGITCPIVPGIMPINNYKGFIRMTGFCKTKIPADIM 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF105995;
AF105996;
                                                                                                                                                                                                                                                                                                                                                          PF02219; MTHFR; 1.
AMS; TIGR00677; fadh2_euk; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF105997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               structure of human and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P00394;
                                                                                                                                                                                 Similarity
                                                                                                                                               Conservative
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AAD20313.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mthfr.
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                                                                                                                                                                             43.18;
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Last annotation updat
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Pred. No. 4.5e-69;
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Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                    12AD31B06B371E17 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                               Mismatches
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                                                                                                                                                                                                          Length 654;
                                                                                                                                            Indels
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                                                                                                       01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence
15-JUN-2002 (Rel. 41, Last annotati
Probable methylenetetrahydrofolate
spaC56F8.10
                                                                  Nature 415:871-880(2002).
-!- CATALYTIC ACTIVITY: 5-methyltetrahydrofolate + NADP(+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MTHR_SCHPO
Q10258;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4896;
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                                              methylenetetrahydrofolate + NADPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FNVWKDEAFEIWSRGWASLYPEDEASRKLVEEVGGSHFLVSLVDNDY-INGDLFAVFAD
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(Rel. 34, Last sequence update)
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AC 15-JUN
DT 15-JUN
DT 15-JUN
DT CABOOK
COCCEURATY
OC EURATY
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OX NCBI_T
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15-JUL-1999 (Rel. 38, Created)
15-JUN-2002 (Rel. 41, Last seq
15-JUN-2002 (Rel. 41, Last ann
       REVISIONS
                            Submitted
                                                  STRAIN-Bristol
                                                             SEQUENCE FROM
                                                                                    NCBI_TaxID=6239;
                                                                                             Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
                                                                                                                  Caenorhabditis elegans.
                                                                                                                                  C06A8.1.
                                                                                                                                            Probable methylenetetrahydrofolate
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InterPro; IPRO03171; Mehydrof_redctse.
Pfam; PF02219; MTHFR; 1.
TIGRFAMs; TIGRO0677; fadh2_euk; 1.
Oxidoreductase; Flavoprotein; FAD; NADP.
SEQUENCE 603 AA; 69012 MW; 38519FEE7
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the European Bioinformatics Institute. There are no restrictions on its
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                            SFLAWKDEAYSL-GMEWANAYSPDSISRKLLVSMMKEWFLCVIVDNDFQNGQSLFDVF
                                                                                                                                                                                                                                                                               SFNVWKDEAFEIWSRGWASLYPEDEASRKLVEEVGGSHFLVSLVDNDYING-DLFAVF
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                                                                                                        Nematoda; Chromadorea;
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45.2%; Pr
tive 57;
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Last annotation update)
rahydrofolate reductase
                           the
                                                                                               Caenorhabditis
                         EMBL/GenBank/DDBJ
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Pred. No. 3.3e-65;
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p53128; Q92318;
D1-OCT-1996 (Rel. 34, Created)
O1-OCT-1996 (Rel. 34, Last sequence update)
O1-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Methylenetetrahydrofolate reductase 2 (EC 1.5.1.20).
MET13 OR MET11 OR VET11 OR VET11 OR VET11 OR VET11 OR SECHATOMYCES CEREVISIAE (Baker's yeast).
Saccharomycetales; Saccharomycotina; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccha
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Submitted (MAY-2002) to the EMBL/GenBank/DDBJ dat
-i- CATALYTIC ACTIVITY: 5-methyltetrahydrofolate
-i- methylenetetrahydrofolate + NADPH.
-i- COEACTOR: FAD (BY SIMILARITY).
-i- PATHWAY: Folate metabolism.
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TIGRFAMS; TIGR00677; fadh2_euk;
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Pfam; PF02219; MTHFR; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GALSDY---QFMRPRARDKKLVEEWAVPLKSVEDIYERFRLYCLG------KLRSNPWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGDRV---FPWKNRSQHPIRCLESVRPIYWSFRPRSYITRTRDWDQFPNGRWGNSSSPAF
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5; Mismatches
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EA94806A2C3BC1CD CRC64;
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Best Local
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SEQUENCE FROM N.A.
MEDLINE-97051592; PubMed-8896269;
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sequence analysis of a 6
Yeast 12:1047-1051(1996)
MTHS_SCHPO STI
074927; P78770; Q1
15-JUL-1999 (Rel.
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or send an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oxidoreductase; Flavoprotein; CONFLICT 73 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF02219; MTHFR; 1.
TIGRFAMS; TIGR00677; fadh2_euk; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR004621; Fadh2_euk.
InterPro; IPR003171; Mehydrof_redotse.
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                                         SCHPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way lified and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          methylenetetrahydrofolate + NAI
COFACTOR: FAD (BY SIMILARITY).
PATHWAY: Folate metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE METHYLENETETRAHYDROFOLATE REDUCTASE (EC 1.5.1.20/\text{EC} 1.7.99.5) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Z72647;
; X94106;
; P00394;
                                                                                                                                                                                                                              QPETKIINEQLEKINTKGFLTINSQPAVNGEKSDSPTVGWGGPGGYVYQKAYVEFFCSKE
                                                                                                                                                                                                                                                                                                                                                                                                  EPIKDNEEAVKAYGIHLGTEMCKKILAHG-IKTLHLYTLNMEKSALAILMNLGLI-EESK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                         IITQMFYDVDNLLNWCSQVRAAGMDVPIIPGIMPITTYAAFLRRIQWGQISIPQHFSSRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IVTQLFYDTDIFLKFVNDCRQIGITCPIVPGIMPINNYKGFIRMTGFCKTKIPADIMAAL 63
                                                                                                                                                                                                                                                                                                                                                                                  S0003093; MET13.
                                                                                                LAWKEEFYHILNEWKLNMNKYDKPHSAQFIQSLIDDYCLVNIVDNDYISPD
                                                                                                                  NVWKDEAFEIWSRGWASLYPEDEA-SRKLVEEVGGSHFLVSLVDNDYINGD
                                                                                                                                                        KLPKLIDTLKNNEFLTYFAIDSQGDLLSNHPDNSKSNAVTWGIFPGREILQPTIVEKISF
                                                                                                                                                                               KLDALVDKCKDRTSLTYMAVNKDGSWKSN-VGQTDVNAVTWGVFPAKEIIQPTIVDPVSF
                                                                                                                                                                                                              NDEINPIKAHLIELNQHSIITINSQPQVNGIRSNDKIHGWGPKDGYVYQKQYLEFMLPKT
                                                                                                                                                                                                                                                                      FGDLDLCGSD--LIRQSA--NKCLELWSTP-TSINDVAFLVINYLNGNLKCLPWSDIP-I
                                                                                                                                                                                                                                                                                               YGAL----SDYQFMRPRARDKKLYEEWAVPLKSYEDIYERFRLYCLGKLRSNPWSELDGL
                                                                                                                                                                                                                                                                                                                              FNAHPLAVLPWRKSLNPKRKNEEVRPIFWKRRPYSYVARTSQWAVDEFPNGRFGDSSSPA
                                                                                                                                                                                                                                                                                                                                                       VSRS----LPWRRPANVFRVKEDVRPIFWANRPKSYISRTIGW--DQYPHGRWGDSCNPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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; 1B5T.
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             STANDARD;
 38, Created)
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Pred. No. 1
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A -> R (IN REF. 1;
AD3465BB52A4E700
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RX MEDLINE=21848401; PubMed=11859360;
RA MEDLINE=21848401; PubMed=11859360;
RA Good V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Gentles S., Goble A., Hamilin N., Harris D., Heddgson G.,
RA Gentles S., Goble A., Hamilin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Money P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Roliver K., O'Nell S., Pearson D., Quall M.A., Rabbinowitsch E.,
RA Rakelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moseft D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT Isla 415:871-880(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Fungi; Ascomycota; Schizosaccharomycete
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Methylenetetrahydrofolate reductase 2
MTHFR2 OR SPAC343.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                  use by non-profit institutions as long as modified and this statement is not removed. But entities requires a license agreement (See htt or send an email to license@isb-sib.ch).
                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                              DNA Res. 4:363-369(1997).

-i- CATALYTIC ACTIVITY: 5-methyltetrahydrofolate
-i- cofaCTOR: FAD (BY SIMILARITY).
-i- PATHWAY: Folate metabolism.
                                    EMBL; AJ011686; CAA09738.1;
EMBL; AL109739; CAB52273.1;
EMBL; D89118; BAA13780.1; -.
HSSP; P00394; 1B5T
                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98162722; PubMed=9501991;
Yoshioka S., Kato K., Nakai K., C
"Identification of open reading f
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-PR745
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                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE METHYLENETETRAHYDROFOLATE (EC 1.5.1.20/\mathrm{EC} 1.7.99.5) FAMILY.
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[nterPro;

IPR004621; IPR003171;

Fadh2\_euk. Mehydrof\_redctse

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MTHR_YEAST
ID MTHR_Y
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DT 01-OCT
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DE Methyl
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Best Local Similarity
Matches 147; Conser
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Bussey H., Storms R.K., Ahmed A., Albermann K., Allen E., Ansor Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V., Botstein D., Bowman S., Bruckner M., Carpenter J., Cherry J.M., Chung E., Churcher C.M., Coster F., Davis K., Davis R.W., Dietrich F.S., Delius H., DiPaolo T., Dubois E., Ducata M., Floeth M., Fortin N
                                                                                                                                                                                                                                                                              MTHR_YEAST
P46151;
                                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
Methylenetetrahydrofolate reductase 1 (EC 1
                                                                                                                                                                Eukaryota; Fungi; Ascomycota; Saccharomycetales; Saccharomycetales
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                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
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                                                                                                                                                                                                                                                                                                                                                                  E-WANLYSKNTPSRKLLENCINDRWLVTVIHHDFMD
                                                                                                                                                                                                                                                                                                                                                                                                                                       RTSLTYMAVNKDGSWKSNVGQTDVNAVTWGVFPAKEIIQPTIVDPVSFNVWKDEAFEIWS
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TIGR00677; fadh2.
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641 AA;
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72140
                                                                                                                                                                 Saccharomycetaceae; Saccharomyces
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G -> A (IN REF. 3).

A -> V (IN REF. 3).

OVTYYAGNNKSEFLTUNPKDGASAVTWGVYPGREIIOSTII
AEVSFKAWLSESFQVWGEWANLYSKNTPSRKLLENCINDRW
LTTYIHHDEMDKNGLWKYLEIDF -> HVRSNESSSISDST
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Pred. No. 1.6e-43;
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                                                                                                                                                                             Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                             PRT;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mapping and mutation identification.";
Nat. Genet. 7:195-200(1994).
-!- CATALYTIC ACTIVITY: 5-methyltetrahydrofolate
    methylenetetrahydrofolate + NADPH.
-!- COPACTOR: FAD (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                            Oxidoreductase; CONFLICT 110
                                                                                                                                                                                                                                                                                                                    SGD; S0005944; MET12.
Interpro; IPR004621; Fadh2_euk.
Interpro; IPR003171; Mehydrof_redctse.
Pfam; PF02219; MTHER; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced between the Swiss Institute of Bioinformatics and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matthews R.G., Rozen R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Goyette P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95004587; PubMed=7920641;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae RAD1 gene.";
Mol. Cell. Biol. 4:2161-2169(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-131 FROM N.A. MEDLINE-85061207; Pubmed-6095044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The nucleotide sequence of Saccharomyces Nature 387:103-105(1997).
                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                            HSSP;
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                                                                                                                                                                                                                                                                                                          TIGRFAMs;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Human methylenetetrahydrofolate reductase:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IDENTIFICATION
303
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European Bioinformatics Institute
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                                                                                                                           ARVIVTQLEYDTDIFLKFVNDCRQ-IGITCPIVPGIMPINNYKGFIRMTGFCKTKIPADI
VLSHIVNESSEEEGEDETSGEIGSIENVPIEDADGDIVLDDSNEETVANRKR---RRHSSL
                                                    LSRFPPEIQSDDNAVKSIGVDILIELIQEIYQRTSGRIKGFHFYTLNLEKAIAQIVSQSP
                                                                                                          ADFVITQLFYDVEKFLTFEMLFRERISQDLPLFPGLMPINSYLLFHRAAKLSHASIPPAI
                                                                               MAALEP-IKDNEEAVKAYGIHLGTEMCKKI----LAHGIKTLHLYTLNMEKSALAILM---
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K02070; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                              Similarity
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657
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73941
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119
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oprotein; FAD; NADP.
oprotein; FAD; NAL (IN REF. 2).
ll D -> VV (IN REF. 2).
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Pred. No. 2.
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2.1e-39;
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                          EESKVSRSLPWRRPANV
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RESULT
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             Query Match
Best Local Similarity
   Matches
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                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaborate between the Swiss Institute of Bioinformatics and the EMBL outstatithe European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commence modified and this statement is not removed. Usage by and for commence modified and this statement is not removed.
                                                                                                                   InterPro; IPR004620;
InterPro; IPR003171;
Pfam; PF02219; MTHFR;
                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                       Oxidoreductase; Flavoprotein; FAD; Methionine biosynthesis;
                                                                                                                                                                 EMBL; AE000740; AAC07387.1; -. HSSP; P00394; 1B5T.
                                                                                                                                                                                                                                                                                                                                                                             aeolicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L. Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Hube Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
"The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    METF OR AQ_1429.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               METF_AQUAE
067422;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Aquificae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
5,10-methylenetetrahydrofolate reducta
                                                                                                        IGRFAMs; TIGR00676; fadh2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=63363;
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                                                                                                                                                                                                                                                                                                                              PATHWAY: Methionine biosynthesis.
SIMILARITY: BELONGS TO THE METHYLENETETRAHYDROFOLATE REDUCTASE (EC 1.5.1.20/EC 1.7.99.5) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTIIEEESFKAWRDEAFSIWSE-WAKLFPRNTPANILLRLVHKDYCLVSIVHHDFKETD
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296 AA;
 Conservative
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             10.2%;
                                                           33871 MW;
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17;
            Score 222;
Pred. No. 7
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                                                           E497CC6CAC9FAFC0 CRC64;
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Mismatches
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                             DB 1;
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                           Length 296;
Indels
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Gaps
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METF_HAEIN
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AC P45208
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METF_STRLI
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Best Local
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Pfam; PF02219; MTHFR; 1.
TIGRFAMs; TIGR00676; fadh2; 1.
Oxidoreductase; Flavoprotein; FAD; Methionine biosynthesis.
SEQUENCE 307 AA; 33267 MW; OCA09C336036D8A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Blanco J., Coque J.R., Martin J.;
"The folate branch of the methionine biosynthesis
Streptomyces lividans: disruption of the 5,10-
methylenetetrahydrofolate reductase gene leads to
METF_HAEIN P45208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             auxotrophy.";
J. Bacteriol. 180:1586-1591(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: BELONGS TO THE METHYLENETETRAHYDROFOLATE REDUCTASE
(EC 1.5.1.20/EC 1.7.99.5) FAMILY.
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15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
5_10-methylenetetrahydrofolate reductase (BC
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                                                                                                 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATALYTIC ACTIVITY: 5-methyltetrahydrofolate + acceptor = methylenetetrahydrofolate + reduced acceptor.

COFACTOR: FAD (BY SIMILARITY).

PATHWAY: Methionine biosynthesis.
                                                                                                 TAKDDPAAVRSIGIEFATEFCARLLAEGVPGLHFITLNNSTATLEIYENLGL
                                                                                                                               PIKDNEEAVKAYGIHLGTEMCKKILAHGIKTLHLYTLNMEKSALAILMNLGL 116
                                                                                                                                                                ITQMFFQPDSYLRLRDRVAAAGCATPVIPEVMPVTSVKMLERLPKLSNASFPAELKERIL
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                                                                                                                                                                                                                                 l Similarity 37; Conser
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                                                                                                                                                                                                                                 Conservative
                 STANDARD;
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                                                                                                                                                                                                                                              8.8%;
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                                                                                                                                                                                                                               Score 193; DB 1;
Pred. No. 1.8e-08;
2; Mismatches 53;
                 PRT;
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                 292
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ETF_ECOLI

ID METF_ECOLI
STANL...

AC P00394;

DT 21-UUL-1986 (Rel. 01, Created)

DT 21-UUL-1986 (Rel. 01, Last sequence update)

DT 15-UUR-2002 (Rel. 41, Last annotation update)

DE 5,10-methylenetetrahydrofolate reductase (EC 1.7.99.5).

METF OR B3941.
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METF_EC
ID ME
AC PO
DT 21
DT 21
DT 11
DT 11
GN M
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Best Local S
Matches 38
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HSSP; P00394;
TIGR; HI1444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rd.";
Science 269:496-512(1995).
--- CATALYTIC ACTIVITY: 5-methyltetrahydrofolate
--- CATALYTIC ACTIVITY: 5-methyltetrahydrofolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-Rd / KW20 / ATCC 51907;
MEDLINE-9535630; PubMed-7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weldman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
"Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content use by non-profit institutions are long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUN-2002 (Rel. 32, Last sequence update)
5,10-methylenetetrahydrofolate reductase (EC METF OR HI1444.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR004620; Fadh2_bact.
InterPro; IPR003171; Mehydrof_rc
Pfam; PF02219; MTHFR; 1.
TIGRPAMS; TIGR00676; fadh2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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01-NOV-1995 (Rel. 32, Last seg
15-JUN-2002 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oxidoreductase; Flavoprotein; FAD; Methionine biosynthesis;
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STRAIN-Rd / KW20 / ATCC
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Bacteria; Proteobacteria;
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COFACTOR: FAD (BY SIMILARITY)
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SEQUENCE 296 AA; 33102 MW; I
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the European Bioinformatics Institute. There
use by non-profit institutions as long as a
modified and this statement is not removed. Us
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InterPro; IPR003171; Mehydrof_redctse
Pfam; PF02219; MTHER; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- COFACTOR: FAD.-!- PATHWAY: Methionine biosynthesis.-!- SUBUNIT: HOMOTETRAMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Guenther B.D., Sheppard C.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=93347969; pubMed=8346018;
Plunkett G. III, Burland V.D., Daniels D.I.
"Analysis of the Escherichia coli genome.
region from 87.2 to 89.2 minutes.";
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"Nucleotide sequence of metF, the E. colimethylene tetrahydrofolate reductase and Nucleic Acids Res. 11:6723-6732(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The structure and properties from Escherichia coli suggest
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli.
Bacteria; Proteobacteria;
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BL; L19201; AAB03073.1; -.
BL; AE000468; AAC76923.1; -.
R; A00462; RDECMH.
R; S40884; S40884
B; 1B5T; 20-JAN-99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . Struct. Biol. 6:359-365(1999).
CATALYTIC ACTIVITY: 5-methyltetrahydrofolate
methylenetetrahydrofolate + reduced acceptor
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GLDDDAETRKLVGANIAMDMVKILSREGVKDFHFYTLNRAEMSYAICHTLGV
                                        PIKDNEEAVKAYGIHLGTEMCKKILAHGIKTLHLYTLNMEKSALAILMNLGL
                                                                                        ITQFFFDVESYLRFRDRCVSAGIDVEIIPGILPVSNFKQAKKFADMTNVRIPAWMAQMFD
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Stauffer G.V., Stauffer L.T.;
"Cloning and nucleotide sequence of
metF gene and its homology with the
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
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CONFLICT
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Bacteria; Proteobacteria;
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InterFro; IPR004620; Fadh2_bact.
InterFro; IPR003171; Mehydrof_redctse.
Pfam; PF02219; MTHFR; 1.
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MEDLINE=21534948; PubMed=11677609;
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SIMILARITY: BELONGS TO THE METHYLENETETRAHYDROFOLATE (EC 1.5.1.20/EC 1.7.99.5) FAMILY.
                                                                                        VTQLFYDTDIFLKFVNDCRQIGITCPIVPGIMPINNYKGFIRMTGFCKTKIPADIMAALE
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PIKDNEEAVKAYGIHLGTEMCKKILAHGIKTLHLYTLNMEKSALAILMNLGL
                                                      ITQFFFDVESYLRFRDRCVSAGIDVEIIPGILPVSNFKQAKKFADMTNVRIPSWMSLMFE
                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                             proteome.
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                                                                                                                                                                                                                                                                      94
296 AA;
                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                      94 A
33173 MW;
                                                                                                                                                                                    8.4%;
                                                                                                                                                                                                                                                                                                                                                                                   fadh2; 1.
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                                                                                                                                                             26;
                                                                                                                                                                                                                                                                                                A
                                                                                                                                                             Score 184; DB 1; I
Pred. No. 9.4e-08;
6; Mismatches 51;
                                                                                                                                                                                                                                                                         2B834F880B56A643 CRC64;
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                                                                                                                                                                                                                   Length 296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           serovar Typhimurium
                                                                                                                                                                Indels
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                      METF_ERWCA
                                RESULT 14
METF_ER P71319;
                                                                 241 GLDNDAETRKLVGANIAMDMVKILSREGVKDFHFYTLNRAEMSYAICHTLGV
           ERWCA
           STANDARD;
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RESULT 15
METF_BUCAI
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P57154;
16-OCT-2001 (
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                                                                                                                                                                                                                        BUCAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib or send an email to license@isb-sib.ch).
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Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
-i- CATALYTIC ACTIVITY: 5-methyltetrahydrofolate + accepmethylenetetrahydrofolate + reduced acceptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam, PF02219; MTHER; 1.
TIGREAMS; TIGRO0676; fadh2; 1.
Oxidoreductase; Flavoprotein; FAD; Methionine biosynthesis.
SEQUENCE 298 AA; 33589 MW; 50FE729E4E3E2C56 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content use by non-profit institutions as long as its content
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symbiotic bacterium).
Bacteria; Proteobacteria;
                                           Buchnera aphidicola (subsp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U74302; AAC72242.1; -. HSSP; P00394; 1B5T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Erwinia carotovora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
5,10-methylenetetrahydrofolate reductase (EC
                                                                     METF OR BU046
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InterPro; IPR003171; Mehydrof_redctse.
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                                                                                       6-OCT-2001 (Rel. 40, Last sequence update, 5-JUN-2002 (Rel. 41, Last annotation update, 10-methylenetetrahydrofolate reductase (
                                                                                                                                                                                                                                                                                                             241
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PATHWAY: Methionine biosynthesis.

SIMILARITY: BELONGS TO THE METHYLENETETRAHYDROFOLATE REDUCTASE
(EC 1.5.1.20/EC 1.7.99.5) FAMILY.
                                                                                                                                                                                                                                                                                                             GLDNDPETRKMVGASIAMDMVKILSREGVKDFHFYTLNRAELSYAICHTLGV
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(Rel. 40,
(Rel. 41,
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ilarity 30.4%;
Conservative 2
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                                              Acyrthosiphon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 176; DB 1;
Pred. No. 4.3e-07
5; Mismatches 5
                                                                                                                                                                                                      PRT;
    subdivision; Buchnera
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ase (EC
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                                              pisum) (Acyrthosiphon
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Best Local S
Matches 34
                                                                                                                                                                                                                                                                                                                        EMBL; AP001118; BAB12769.1; -.
HSSP; P00394; 1B5T.
InterPro; IPR004620; Fadh2_bact.
InterPro; IPR003171; Mehydrof_redctse.
InterPro; IPR003171; Mehydrof_redctse.
Pfam; PF02219; MTHFR; 1.
TIGRFAMS; TIGR00676; fadh2; 1.
OXIdoreductase; Flavoprotein; FAD; Methionine biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                         Complete proteome. SEQUENCE 292 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
"Genome sequence of the endocellular bacterial symbiont of aphids
Buchnera sp. APS.";
Nature 407:81-86(2000).

1 CATALYTIC ACTIVITY: 5-methyltetrahydrofolate + acceptor = 5,10-
methyl-neneteriahydrofolate + reduced acceptor.

1 COFACTOR: FAD (BY SIMILARITY).

1 PATHWAY: Methionine biosynthesis.

1 SIMILARITY: BELONGS TO THE METHYLENETETRAHYDROFOLATE REDUCTASE
(EC 1.5.1.20/EC 1.7.99.5) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN-Tokyo 1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20445173; PubMed=10993077;
                                                                                                                                       241 GLDDDIFTQKIIGSSIAIDMVKKLSCEGVKNFHFYTLNQSDITYSICHILGL 292
                                                                                    ch 7.7%; Score 168; DB 1; L-
1 Similarity 30.4%; Pred. No. 1.9e-06;
34; Conservative 24; Mismatches 54;
                                                                                                                                                                                                                                                                                     33730 MW; 1D2A9E1B4D6E0DA9 CRC64;
                                                                                                                                                                                                                                                   Length 292;
                                                                                                                                                                                                                Indels
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